

09/863600

FILE 'REGISTRY' ENTERED AT 12:25:15 ON 06 NOV 2003
L1 4 S GGTASCHFGPLTWVCKPQGG/SQSP

L1 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 243125-13-5 REGISTRY
CN Glycinamide, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteinyl-L-histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-tryptophyl-L-valyl-L-cysteinyl-L-lysyl-L-prolyl-L-glutaminyglycyl-, cyclic (6→15)-disulfide (9CI) (CA INDEX NAME)
SQL 20

SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 131:209282

L1 ANSWER 2 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 209594-31-0 REGISTRY
CN Glycinamide, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteinyl-L-histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-tryptophyl-L-valyl-L-cysteinyl-L-lysyl-L-prolyl-L-glutaminyglycyl-, (9CI) (CA INDEX NAME)
SQL 20

SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 129:90879

L1 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 203397-46-0 REGISTRY
CN Glycine, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteinyl-L-histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-tryptophyl-L-valyl-L-cysteinyl-L-lysyl-L-prolyl-L-glutaminyglycyl-, cyclic (6→15)-disulfide (9CI) (CA INDEX NAME)
SQL 20

SEQ 1 GGTASCHFGP LTWVCKPQGG
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 128:176424

L1 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2003 ACS on STN
RN 186526-47-6 REGISTRY
CN Glycine, glycylglycyl-L-threonyl-L-alanyl-L-seryl-L-cysteinyl-L-histidyl-L-phenylalanylglycyl-L-prolyl-L-leucyl-L-threonyl-L-tryptophyl-L-valyl-L-cysteinyl-L-lysyl-L-prolyl-L-glutaminyglycyl-, (9CI) (CA INDEX NAME)
OTHER NAMES:

09/863600

CN 13: PN: WO0191780 SEQID: 19 claimed protein
SQL 20

SEQ 1 GGTASCHFPG LTWVCKPQGG

HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:32169

REFERENCE 2: 130:61259

REFERENCE 3: 130:493

REFERENCE 4: 126:152802

FILE 'HCAPLUS' ENTERED AT 12:26:08 ON 06 NOV 2003
L2 7 S L1

L2 ANSWER 1 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:885800 HCAPLUS

DOCUMENT NUMBER: 136:32169

TITLE: Neuroprotective peptides that are peptide
mimetics of erythropoietin

INVENTOR(S): Smith-Swintosky, Virginia; Renzi, Michael;
Plata-Salaman, Carlos; Jolliffe, Linda; Farrell,
Francis; Johnson, Dana L.

PATENT ASSIGNEE(S): Ortho-McNeil Pharmaceutical, Inc., USA

SOURCE: PCT Int. Appl., 75 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001091780	A1	20011206	WO 2001-US16654	20010523
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1296702	A1	20030402	EP 2001-941562	20010523
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
US 2003130197	A1	20030710	US 2001-863600	20010523
PRIORITY APPLN. INFO.:			US 2000-207654P P	20000526
			WO 2001-US16654 W	20010523

OTHER SOURCE(S): MARPAT 136:32169

AB Methods of treating diseases of the nervous system by administration

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of compns. having the neurol. therapeutic activity of human erythropoietin are disclosed. These compns. include therapeutic agents such as peptides, peptide dimers, polypeptides, and proteins that have the full range of biol. activity of human erythropoietin or only certain biol. activities of erythropoietin. Improved therapeutic regimens where the erythropoietin is administered at concns. below those required to stimulate hematopoiesis are also provided.

IT 186526-47-6

RL: PAC (Pharmacological activity); BIOL (Biological study)
(neuroprotective peptides that are peptide mimetics of erythropoietin)

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR
THIS RECORD. ALL CITATIONS AVAILABLE IN
THE RE FORMAT

L2 ANSWER 2 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:396628 HCAPLUS

DOCUMENT NUMBER: 131:209282

TITLE: A peptide mimetic of erythropoietin: critical residues and description of a minimal functional epitope

AUTHOR(S): Johnson, Dana L.; Farrell, Francis X.; McMahon, Frank J.; Tullai, Jennifer; Barbone, Francis P.; Middleton, Steven A.; Hoey, Kenway; Livnah, Oded; Wrighton, Nicholas C.; Dower, William J.; Mulcahy, Linda S.; Stura, Enrico A.; Wilson, Ian A.; Jolliffe, Linda K.

CORPORATE SOURCE: Drug Discovery Research, The R. W. Johnson Pharmaceutical Research Inst., Raritan, NJ, USA

SOURCE: Peptides: Frontiers of Peptide Science, Proceedings of the American Peptide Symposium, 15th, Nashville, June 14-19, 1997 (1999), Meeting Date 1997, 501-503. Editor(s): Tam, James P.; Kaumaya, Pravin T. P. Kluwer: Dordrecht, Neth.
CODEN: 67UCAR

DOCUMENT TYPE: Conference

LANGUAGE: English

AB Ala substitution in the conserved positions of EMP1 (GGTYSCHFGPLTWCKPQGG), a peptide mimetic of erythropoietin, was done to determine the effect on both binding and mimetic activity in vitro. Most of the Ala substitutions decreased the relative binding affinity. Trp13 substitution had the most significant effect, resulting in almost undetectable binding and a complete loss of mimetic activity. Ala substitution of Tyr4, Gly9 or Thr12 each resulted in significant relative binding losses and a concomitant loss of mimetic action. Unexpectedly, Ala substitution of Pro10 had no effect on relative binding or mimetic activity suggesting that an acceptable β -turn structure can still be achieved. Substitution of Pro17 resulted in a 100-fold loss of mimetic activity. The relative binding of this peptide was also significantly altered and was limited by decreased peptide solubility. The two aromatic residues at positions Tyr4 and Trp13 appear to play important roles in both EPO receptor binding ability and EPO mimetic properties of EMP1. To investigate this further, Tyr4 or Trp13 was replaced with Phe. Restoration of aromaticity at position 4 resulted in the recovery of some binding activity (12-fold less than

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EMP1) and mimetic activity. Restoration of aromaticity at Trp13 resulted in recovery of activity to a level similar to EMP1. The data indicate that aromatic residues at these positions are important for EMP1 agonist activity. The authors next sought to determine the minimal active structure within the EMP1 sequence by truncating residues of the peptide outside the disulfide bond. YSCHFGPLTWVCK represents the minimal active structure identified.

IT 243125-13-5

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(peptide mimetic of erythropoietin, its critical residues and description of a minimal functional epitope)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:730721 HCAPLUS

DOCUMENT NUMBER: 130:61259

TITLE: An antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation

AUTHOR(S): Livnah, Oded; Johnson, Dana L.; Stura, Enrico A.; Farrell, Francis X.; Barbone, Francis P.; You, Yun; Liu, Kathleen D.; Goldsmith, Mark A.; He, Wen; Krause, Christopher D.; Pestka, Sidney; Jolliffe, Linda K.; Wilson, Ian A.

CORPORATE SOURCE: Department of Molecular Biology and the Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, 92037, USA

SOURCE: Nature Structural Biology (1998), 5(11), 993-1004

CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER: Nature America

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Dimerization of the erythropoietin (EPO) receptor (EPOR), in the presence of either natural (EPO) or synthetic (EPO-mimetic peptides, EMPs) ligands is the principal extracellular event that leads to receptor activation. The crystal structure of the extracellular domain of EPOR bound to an inactive (antagonist) peptide at 2.7 Å resolution has unexpectedly revealed that dimerization still occurs, but the orientation between receptor mols. is altered relative to active (agonist) peptide complexes. Comparison of the biol. properties of agonist and antagonist EMPs with EPO suggests that the extracellular domain orientation is tightly coupled to the cytoplasmic signaling events and, hence, provides valuable new insights into the design of synthetic ligands for EPOR and other cytokine receptors.

IT 186526-47-6

RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(EPO-mimetic peptides; antagonist peptide-EPO receptor complex suggests that receptor dimerization is not sufficient for activation)

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE

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FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 4 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:719126 HCAPLUS

DOCUMENT NUMBER: 130:493

TITLE: Methods of administering peptides that bind to
the erythropoietin receptor, and method for
therapeutic use

INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang,
Ray S.; Kashyap, Arun K.

PATENT ASSIGNEE(S): Affymax Technologies N.V., UK

SOURCE: U.S., 103 pp., Cont.-in-part of U.S. Ser. No.
155,940, abandoned.

CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5830851	A	19981103	US 1995-484631	19950607
CA 2223833	AA	19961219	CA 1996-2223833	19960607
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA			
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
CN 1192748	A	19980909	CN 1996-196094	19960607
EP 886648	A1	19981230	EP 1996-919296	19960607
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1993-155940	B2 19931119
			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 130:493

AB Peptides of 10 to 40 or more amino acid residues in length and having the sequence X3X4 X5GPX6TWX7X8 (X3 = C; X4 = R, H, L, W; X5 = M, F, I; X6 = any of 20 genetically coded L-amino acids; X7 = D, E, I, L, V; X8 = C), which bind and activate the erythropoietin receptor (EPO-R) or otherwise act as an EPO agonist, are provided, as are methods for their use in treating a patient with a deficiency of erythropoietin or a low or defective red blood cell population.

IT 186526-47-6

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptides binding to erythropoietin receptor, and therapeutic

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use)
REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 5 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1998:430094 HCAPLUS
DOCUMENT NUMBER: 129:90879
TITLE: Peptide ligands for the erythropoietin receptor
that act as erythropoietin agonists
INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang,
Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.;
Johnson, Dana; Mulcahy, Linda
PATENT ASSIGNEE(S): Affymax Technologies N.V., UK
SOURCE: U.S., 103 pp., Cont.-in-part of U. S. Ser. No.
155,940, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5773569	A	19980630	US 1995-484635	19950607
CA 2223833	AA	19961219	CA 1996-2223833	19960607
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA			
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
CN 1192748	A	19980909	CN 1996-196094	19960607
EP 886648	A1	19981230	EP 1996-919296	19960607
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
US 5986047	A	19991116	US 1997-827570	19970328
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1993-155940	B2 19931119
			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 129:90879

AB Peptides of 10 to 40 or more amino acids that bind and activate the erythropoietin receptor (EPO-R) or otherwise act as an EPO agonist for therapeutic uses are described. Peptides were identified by screening of libraries prepared using degenerate oligonucleotides to construct a phage display library that was screened by panning with the receptor. Candidate peptides were synthesized as C-terminal amide derivs by standard Fmoc on PAL resins and tested for biol. activity. Many peptides showed greater affinity for the receptor than did erythropoietin.

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IT 209594-31-0

RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); PRP (Properties); BIOL (Biological
study)

(amino acid sequence; peptide ligands for erythropoietin receptor
that act as erythropoietin agonists)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 6 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1998:129605 HCAPLUS

DOCUMENT NUMBER: 128:176424

TITLE: Identification of a 13 Amino Acid Peptide
Mimetic of Erythropoietin and Description of
Amino Acids Critical for the Mimetic Activity of
EMP1

AUTHOR(S): Johnson, Dana L.; Farrell, Francis X.; Barbone,
Francis P.; McMahon, Frank J.; Tullai, Jennifer;
Hoey, Kenway; Livnah, Oded; Wrighton, Nicholas
C.; Middleton, Steven A.; Loughney, Deborah A.;
Stura, Enrico A.; Dower, William J.; Mulcahy,
Linda S.; Wilson, Ian A.; Jolliffe, Linda K.

CORPORATE SOURCE: R. W. Johnson Pharmaceutical Research Institute
Drug Discovery Research, Raritan, NJ, 08869, USA

SOURCE: Biochemistry (1998), 37(11), 3699-3710

CODEN: BICHAW; ISSN: 0006-2960

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB To obtain information about the functional importance of amino acids
required for effective erythropoietin (EPO) mimetic action, the
conserved residues of a peptide mimetic of EPO, recently discovered
by phage display, were subjected to an alanine replacement strategy.
Further, to identify a minimal mimetic peptide sequence, a series of
truncation peptides has been generated. One EPO mimetic peptide
sequence, EMP1, was targeted and more than 25 derivs. of this
sequence were evaluated for their ability to compete with [125I]EPO
for receptor binding and for their ability to support the
proliferation of two EPO-responsive cell lines. Two hydrophobic
amino acids, Tyr4 and Trp13, appear essential for mimetic action,
and aromatic residues appear to be important at these sites. These
findings are consistent with the previously reported x-ray crystal
structure of EMP1 complexed with the extracellular domain of the EPO
receptor (EPO binding protein; EBP). In the authors' efforts to
define the structural elements required for EPO mimetic action, a 13
amino acid peptide was identified which possesses mimetic properties
and contains a minimal agonist epitope. The ability of this peptide
to effectively serve as a mimetic capable of the induction of
EPO-responsive cell proliferation appears to reside within a single
residue, equivalent to position Tyr4 to EMP1, when present in a sequence
that includes the cyclic core peptide structure. Although these
peptides are less potent than EPO, they should serve as an excellent
starting point for the design of compds. with EPO mimetic activity.

IT 203397-46-0

RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); PRP (Properties); BIOL (Biological
study)

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(identification of a 13 amino acid peptide mimetic of erythropoietin and description of amino acids critical for mimetic activity)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 7 HCAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1997:148850 HCAPLUS

DOCUMENT NUMBER: 126:152802

TITLE: Linear, cyclic, and disulfide dimer synthetic peptides as erythropoietin agonists, binding by erythropoietin receptor, and pharmaceutical uses
INVENTOR(S): Wrighton, Nicholas C.; Dower, William J.; Chang, Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.; Johnson, Dana; Mulcahy, Linda

PATENT ASSIGNEE(S): Johnson and Johnson Corporation, USA; Affymax Technologies, N.V.; Wrighton, Nicholas C.; Dower, William J.; Chang, Ray S.; Kashyap, Arun K.; Jolliffe, Linda K.; Johnson, Dana; Mulcahy, Linda

SOURCE: PCT Int. Appl., 94 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9640749	A1	19961219	WO 1996-US9810	19960607
W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG			
RW:	KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA			
US 5773569	A	19980630	US 1995-484635	19950607
US 5830851	A	19981103	US 1995-484631	19950607
AU 9661667	A1	19961230	AU 1996-61667	19960607
AU 712713	B2	19991111		
EP 886648	A1	19981230	EP 1996-919296	19960607
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
JP 11507367	T2	19990629	JP 1996-502023	19960607
BR 9609006	A	19991214	BR 1996-9006	19960607
PL 185040	B1	20030228	PL 1996-323858	19960607
NO 9705729	A	19980205	NO 1997-5729	19971205
PRIORITY APPLN. INFO.:			US 1995-484631	A 19950607
			US 1995-484635	A 19950607
			US 1993-155940	B2 19931119
			WO 1996-US9810	W 19960607

OTHER SOURCE(S): MARPAT 126:152802

AB This invention includes peptides of 10 to 40 or more amino acid residues in length and having the sequence X3X4X5GPX6TWX7X8 where each amino acid is indicated by standard one letter abbreviation; X3 is C; X4 is R, H, L, or W; X5 is M, F, or I; X6 is independently selected from any one of the 20 genetically coded L-amino acids; X7

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is D, E, I, L, or V; and X8is C, which bind and activate the erythropoietin receptor (EPO-R) or otherwise act as EPO agonists, and methods for their use. The peptides are mostly linear, or may be cyclic. Disulfide dimers are also included. These are useful for treating anemia, abnormal erythropoiesis, and other disease states.

IT **186526-47-6**

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(erythropoietin agonist; linear, cyclic, and disulfide dimer synthetic peptides as erythropoietin agonists, binding by erythropoietin receptor, and pharmaceutical uses)

FILE 'HOME' ENTERED AT 12:26:26 ON 06 NOV 2003

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:05:39 ; Search time 171 Seconds
(without alignments)
106.423 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Pending Patents AA Main:
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pcp.*
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27: /cgn2_6/ptodata/1/paa/US101_COMB.pcp.*
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29: /cgn2_6/ptodata/1/paa/US103_COMB.pcp.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pcp.*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pcp.*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	123	100.0	20 12	US-08-827-573-52 Sequence 52, Appl

75 117 95.1 20 27 US-10-156-934-8
76 117 95.1 20 27 US-10-156-934-190
77 117 95.1 20 28 US-10-231-494-11
78 117 95.1 20 28 US-10-231-494-25
79 117 95.1 20 28 US-10-271-869-66
80 117 95.1 20 29 US-10-378-094-11
81 117 95.1 20 31 US-10-609-217-87
82 117 95.1 20 31 US-10-609-217-93
83 117 95.1 20 31 US-10-609-217-1025
84 117 95.1 20 31 US-10-645-761-87
85 117 95.1 20 31 US-10-645-761-93
86 117 95.1 20 31 US-10-645-761-1025
87 117 95.1 20 32 US-60-460-829-11
88 117 95.1 22 1 PCT-US99-25044-97
89 117 95.1 22 18 US-09-428-082-97
90 117 95.1 22 18 US-09-428-082B-97
91 117 95.1 22 19 US-09-563-286B-97
92 117 95.1 22 19 US-09-563-286C-97
93 117 95.1 22 31 US-10-609-217-97
94 117 95.1 22 31 US-10-645-761-97
95 117 95.1 23 1 PCT-US99-25044-94
96 117 95.1 23 1 PCT-US99-25044-98
97 117 95.1 23 12 US-08-827-573-20
98 117 95.1 23 15 US-09-155-158-20
99 117 95.1 23 18 US-09-428-082-94
100 117 95.1 23 18 US-09-428-082-98

ALIGNMENTS

RESULT 1
US-08-827-573-52
; Sequence 52, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-573-52

Query Match 100.0%; Score 123; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
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RESULT 2
US-09-155-158-52
; Sequence 52, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-155-158-52

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Query Match      100.0%; Score 123; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3
US-09-863-600E-19
; Sequence 19, Application US/09863600E
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (OPT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-19

Query Match      100.0%; Score 123; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4
US-10-156-934-52
; Sequence 52, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; CORRESPONDENCE ADDRESS:
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia

Query Match      100.0%; Score 123; DB 27; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 5
US-08-827-573-189
; Sequence 189, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
```


REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-573-189

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. NO. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGLTWCKPQGG 20

RESULT 6
US-08-827-573-247
Sequence 247, Application US/08827573
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-827-573-247

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. NO. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 7
US-08-827-573-248
Sequence 248, Application US/08827573
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-827-573-248

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. NO. 2.6e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 8

US-08-827-573-249
; Sequence 249, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"

US-08-827-573-249

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 9

US-08-827-573-250
; Sequence 250, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,573
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"

US-08-827-573-250

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 10

US-09-155-158-189
; Sequence 189, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.

```
? Johnson, Dana
? Mulcahy, Linda
?
? TITLE OF INVENTION: Compounds and Peptides That Bind to the
? Erythropoietin Receptor
?
? NUMBER OF SEQUENCES: 262
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Affymax Research Institute
? STREET: 4001 Miranda Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/155,158
? FILING DATE: 03-Jun-1999
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US96/09810
? FILING DATE: 07-JUN-1996
? APPLICATION NUMBER: US 08/484,635
? FILING DATE: 07-JUN-1995
? APPLICATION NUMBER: US 08/484,631
? FILING DATE: 07-JUN-1995
? APPLICATION NUMBER: US 08/155,940
? FILING DATE: 19-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Stracker, Elaine C.
? REGISTRATION NUMBER: 43,166
? REFERENCE/DOCKET NUMBER: 1053.3W
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (650) 812-8700
? TELEFAX: (650) 424-0832
?
? INFORMATION FOR SEQ ID NO: 189:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 amino acids
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? SEQUENCE DESCRIPTION: SEQ ID NO: 189:
?
? US-09-155-158-189
?
? Query Match 96.7%; Score 119; DB 15; Length 20;
? Best Local Similarity 95.0%; Pred. No. 2.6e-09;
? Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
?
? Qy 1 GGTASCHFGPLTWCKPQG 20
? Db 1 GGTTSCHFGPLTWCKPQG 20
?
? RESULT 11
? US-09-155-158-247
? Sequence 247, Application US/09155158
? GENERAL INFORMATION:
? APPLICANT: Wrighton, Nicholas C.
? Dower, William J.
? Kashyap, Arun K.
? Johnson, Dana
? Jolliffe, Linda K.
? Mulcahy, Linda
?
? TITLE OF INVENTION: Compounds and Peptides That Bind to the
? Erythropoietin Receptor
?
? NUMBER OF SEQUENCES: 262
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Affymax Research Institute
? STREET: 4001 Miranda Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
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?
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
? ZIP: 94304
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/155,158
? FILING DATE: 03-Jun-1999
? CLASSIFICATION: <Unknown>
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? APPLICATION NUMBER: PCT/US96/09810
? FILING DATE: 07-JUN-1996
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? FILING DATE: 07-JUN-1995
? APPLICATION NUMBER: US 08/484,631
? FILING DATE: 07-JUN-1995
? APPLICATION NUMBER: US 08/155,940
? FILING DATE: 19-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Stracker, Elaine C.
? REGISTRATION NUMBER: 43,166
? REFERENCE/DOCKET NUMBER: 1053.3W
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (650) 812-8700
? TELEFAX: (650) 424-0832
?
? INFORMATION FOR SEQ ID NO: 247:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 amino acids
? TYPE: amino acid
? STRANDEDNESS: <Unknown>
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Modified-site
? LOCATION: 4
? OTHER INFORMATION: /product="OTHER"
? /note="Xaa = para-nitro-phenylalanine"
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 247:
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? US-09-155-158-247
?
? Query Match 96.7%; Score 119; DB 15; Length 20;
? Best Local Similarity 95.0%; Pred. No. 2.6e-09;
? Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
?
? Qy 1 GGTASCHFGPLTWCKPQG 20
? Db 1 GGTXSCHFGPLTWCKPQG 20
?
? RESULT 12
? US-09-155-158-248
? Sequence 248, Application US/09155158
? GENERAL INFORMATION:
? APPLICANT: Wrighton, Nicholas C.
? Dower, William J.
? Chang, Ray S.
? Kashyap, Arun K.
? Jolliffe, Linda K.
? Johnson, Dana
? Mulcahy, Linda
?
? TITLE OF INVENTION: Compounds and Peptides That Bind to the
? Erythropoietin Receptor
?
? NUMBER OF SEQUENCES: 262
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Affymax Research Institute
? STREET: 4001 Miranda Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: USA
```

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;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Jun-1999
; APPLICATION NUMBER: US/09/155,158
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-amino-phenylalanine"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 248:
US-09-155-158-248
Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 13
US-09-155-158-249
; Sequence 249, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Kashyap, Arun K.
; Johnson, Dana
; Jolliffe, Linda K.
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Jun-1999
; APPLICATION NUMBER: US/09/155,158
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-fluoro-phenylalanine"
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 249:
US-09-155-158-249
Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 14
US-09-155-158-250
; Sequence 250, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Kashyap, Arun K.
; Johnson, Dana
; Jolliffe, Linda K.
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/155,158
;/ FILING DATE: 03-JUN-1999
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US96/09810
;/ FILING DATE: 07-JUN-1996
;/ APPLICATION NUMBER: US 08/484,635
;/ FILING DATE: 07-JUN-1995
;/ APPLICATION NUMBER: US 08/484,631
;/ FILING DATE: 07-JUN-1995
;/ APPLICATION NUMBER: US 08/155,940
;/ FILING DATE: 19-NOV-1993
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Stracker, Elaine C.
;/ REGISTRATION NUMBER: 43,166
;/ REFERENCE/DOCKET NUMBER: 1053.3W
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (650) 812-8700
;/ TELEFAX: (650) 424-0832
;/ INFORMATION FOR SEQ ID NO: 250:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ FEATURE:
;/ NAME/KEY: Modified-site
;/ LOCATION: 4
;/ OTHER INFORMATION: /product= "OTHER"
;/ /note= "Xaa = 3,5-dibromo-tyrosine"
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 250:
;/ US-09-155-158-250

Query Match 96.7%; Score 119; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 15
US-09-863-600E-29
;/ Sequence 29, Application US/09863600E
;/ GENERAL INFORMATION:
;/ APPLICANT: Smith-Swintosky, Virginia
;/ APPLICANT: Renzi, Michael
;/ APPLICANT: Plata-Salaman, Carlos
;/ APPLICANT: Jolliffe, Linda
;/ APPLICANT: Farrell, Francis
;/ APPLICANT: Johnson, Dana
;/ TITLE OF INVENTION: Neuroprotective Peptides
;/ FILE REFERENCE: PRI-0014 (ORT-1436)
;/ CURRENT APPLICATION NUMBER: US/09/863,600E
;/ CURRENT FILING DATE: 2001-05-23
;/ PRIOR APPLICATION NUMBER: 60/207,654
;/ PRIOR FILING DATE: 2000-05-26
;/ NUMBER OF SEQ ID NOS: 49
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 29
;/ LENGTH: 20
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Synthetic Peptide
;/ US-09-863-600E-29

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTTSCHFGPLTWCKPQGG 20
RESULT 16
US-09-863-600E-37
;/ Sequence 37, Application US/09863600E
;/ GENERAL INFORMATION:
;/ APPLICANT: Smith-Swintosky, Virginia
;/ APPLICANT: Renzi, Michael
;/ APPLICANT: Plata-Salaman, Carlos
;/ APPLICANT: Jolliffe, Linda
;/ APPLICANT: Farrell, Francis
;/ APPLICANT: Johnson, Dana
;/ TITLE OF INVENTION: Neuroprotective Peptides
;/ FILE REFERENCE: PRI-0014 (ORT-1436)
;/ CURRENT APPLICATION NUMBER: US/09/863,600E
;/ CURRENT FILING DATE: 2001-05-23
;/ PRIOR APPLICATION NUMBER: 60/207,654
;/ PRIOR FILING DATE: 2000-05-26
;/ NUMBER OF SEQ ID NOS: 49
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 37
;/ LENGTH: 20
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Synthetic Peptide
;/ NAME/KEY: misc_feature
;/ LOCATION: (4)..(4)
;/ OTHER INFORMATION: Xaa is D-Tyr
;/ US-09-863-600E-37

Query Match 96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 17
US-09-863-600E-38
;/ Sequence 38, Application US/09863600E
;/ GENERAL INFORMATION:
;/ APPLICANT: Smith-Swintosky, Virginia
;/ APPLICANT: Renzi, Michael
;/ APPLICANT: Plata-Salaman, Carlos
;/ APPLICANT: Jolliffe, Linda
;/ APPLICANT: Farrell, Francis
;/ APPLICANT: Johnson, Dana
;/ TITLE OF INVENTION: Neuroprotective Peptides
;/ FILE REFERENCE: PRI-0014 (ORT-1436)
;/ CURRENT APPLICATION NUMBER: US/09/863,600E
;/ CURRENT FILING DATE: 2001-05-23
;/ PRIOR APPLICATION NUMBER: 60/207,654
;/ PRIOR FILING DATE: 2000-05-26
;/ NUMBER OF SEQ ID NOS: 49
;/ SOFTWARE: PatentIn version 3.2
;/ SEQ ID NO 38
;/ LENGTH: 20
;/ TYPE: PRT
;/ ORGANISM: Artificial Sequence
;/ FEATURE:
;/ OTHER INFORMATION: Synthetic Peptide
;/ NAME/KEY: misc_feature
;/ LOCATION: (4)..(4)
;/ OTHER INFORMATION: Xaa is p-NO2-Phe
;/ US-09-863-600E-38

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US-09-863-500E-40
? Sequence 40, Application US/098635600E
? GENERAL INFORMATION:
? APPLICANT: Smith-Swintovsky, Virginia
? APPLICANT: Renzi, Michael
? APPLICANT: Plata-Salaman, Carlos
? APPLICANT: Jolliffe, Linda
? APPLICANT: Farrell, Francis
? APPLICANT: Johnson, Dana
? TITLE OF INVENTION: Neuroprotective
? FILE REFERENCE: PRI-0014 (ORT-1436)
? CURRENT APPLICATION NUMBER: US/09/86
? CURRENT FILING DATE: 2001-05-23
? PRIOR APPLICATION NUMBER: 60/207,654
? PRIOR FILING DATE: 2000-05-26
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: patentin version 3.2
? SEQ ID NO 40
? LENGTH: 20
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:

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; SEQ ID NO 42
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is 3,5-dibromo-Tyr
US-09-863-600E-42

Query Match          96.7%; Score 119; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 22
US-10-156-934-189
; Sequence 189, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-3700
; TELEFAX: (858) 720-2500
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-nitro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-10-156-934-247
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; SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-10-156-934-189

Query Match          96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 23
US-10-156-934-247
; Sequence 247, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/156,934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hostetler, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 033134.1053.CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = para-nitro-phenylalanine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-10-156-934-247

Query Match          96.7%; Score 119; DB 27; Length 20;
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RESULT 26
US-10-156-934-250
; Sequence 250, Application US/10156934
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Chang, Ray S.
; Kashyap, Arun K.
TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
NUMBER OF SEQUENCES: 267
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/156.934
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/155,158
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
; NAME: Hoetzel, Michael J.
; REGISTRATION NUMBER: 47,664
; REFERENCE/DOCKET NUMBER: 031134.1053.CIP4
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 720-2500
; TELEFAX: (858) 720-3700
INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; /note= "Xaa = 3,5-dibromo-tyrosine"
; SEQUENCE DESCRIPTION: SEQ ID NO: 250:
US-10-156-934-250
Query Match 96.7%; Score 119; DB 27; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.6e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20
RESULT 27
PCT-US02-27637-11
; Sequence 11, Application PC/TUS0227637
; GENERAL INFORMATION:

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; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US02/27637
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
PCT-US02-27637-11
Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 28
PCT-US02-27637-25
; Sequence 25, Application PC/TUS0227637
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-WO
; CURRENT APPLICATION NUMBER: PCT/US02/27637
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
PCT-US02-27637-25
Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 29
PCT-US03-18645-7
; Sequence 7, Application PC/TUS0318645
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Digicayloglu, Murat
; APPLICANT: Lipton, Stuart A.
; TITLE OF INVENTION: Neuroprotective Synergy of
; Erythropoietin and Insulin-Like Growth Factors
; FILE REFERENCE: 66821-216
; CURRENT APPLICATION NUMBER: PCT/US03/18645

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; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,058
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/459,145
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US03-18645-7

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30

PCT-US99-25044-87
; Sequence 87, Application PC/TUS9925044
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: PCT/US99/25044
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:EPO-MIMETIC
; OTHER INFORMATION: PEPTIDE
PCT-US99-25044-87

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 31

PCT-US99-25044-1025
; Sequence 1025, Application PC/TUS9925044
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: PCT/US99/25044
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:EPO MIMETIC
; OTHER INFORMATION: PEPTIDE
PCT-US99-25044-1025

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 32

US-08-155-940A-8
; Sequence 8, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-155-940A-8

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 33

US-08-155-940A-35

```
; Sequence 35, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELEPHONE: 415-424-0832
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-155-940A-35

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 34
US-08-155-940A-49
; Sequence 49, Application US/08155940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELEPHONE: 415-424-0832
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-155-940A-49
```

```
; Sequence 35, Application US/08155,940A
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940A
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELEPHONE: 415-424-0832
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-155-940A-49

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 35
US-08-155-940A-49
; Sequence 8, Application US/08451550
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELEPHONE: 415-424-0832
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-155-940A-49
```

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; MOLECULE TYPE: peptide
US-08-451-550-8

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 36
US-08-451-550-35
; Sequence 35, Application US/08451550
; GENERAL INFORMATION:
; APPLICANT: Chang, Ray S.
; APPLICANT: Dower, William J.
; APPLICANT: Kashyap, Arun K.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V., Administrative Offices
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,550
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 11509-122/1053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-451-550-49

Query Match          95.1%; Score 117; DB 8; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 38
US-08-827-573-8
; Sequence 8, Application US/08827573
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/827,573
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-573-B

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09; 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 39
US-08-827-573-190
Sequence 190, Application US/08827573
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-573-190

Query Match 95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09; 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 40
US-09-052-889-34
Sequence 34, Application US/09052889
GENERAL INFORMATION:
APPLICANT: Clark, Ross G.
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,889
FILING DATE: 31-Mar-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: F1071R1
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-052-889-34

Query Match 95.1%; Score 117; DB 14; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09; 1; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 41
US-09-155-158-8
; Sequence 8, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Kashyap, Arun K.
; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-155-158-8

Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 42
US-09-155-158-190
; Sequence 190, Application US/09155158
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; Dower, William J.
; Kashyap, Arun K.

; Jolliffe, Linda K.
; Johnson, Dana
; Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; Erythropoietin Receptor
; NUMBER OF SEQUENCES: 262
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Research Institute
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,158
; FILING DATE: 03-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09810
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/484,631
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stracker, Elaine C.
; REGISTRATION NUMBER: 43,166
; REFERENCE/DOCKET NUMBER: 1053.3W
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 812-8700
; TELEFAX: (650) 424-0832
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 190:
US-09-155-158-190

Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 43
US-09-189-745-1
; Sequence 1, Application US/09189745
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ian A.
; APPLICANT: Livnah, Oded
; APPLICANT: Stura, Enrico A.
; APPLICANT: Johnson, Dana L.
; APPLICANT: Jolliffe, Linda K.
; TITLE OF INVENTION: SMALL MOLECULE MIMETICS OF
; ERYTHROPOIETIN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston

```
; STATE: WA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/189,745
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/641,071
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07300/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-189-745-1

Query Match 95.1%; Score 117; DB 15; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 44
US-09-341-590-117
; Sequence 117, Application US/09341590
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
; FILE REFERENCE: PPT-20479-US
; FILE REFERENCE: PPT-20479-US
; CURRENT APPLICATION NUMBER: US/09/341,590
; CURRENT FILING DATE: 1999-07-03
; PRIOR APPLICATION NUMBER: DK 0317/98
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 117
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EMP-1
; US-09-341-590-117

Query Match 95.1%; Score 117; DB 17; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45
US-09-428-082-87
; Sequence 87, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SPO MIMETIC
; US-09-428-082-1025

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47
US-09-428-082B-87
; Sequence 87, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
```

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; Sequence 87, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO-MIMETIC
; US-09-428-082-87

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 46
US-09-428-082-1025
; Sequence 1025, Application US/09428082
; GENERAL INFORMATION:
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: FEIGE, ULRICH
; APPLICANT: CHEETHAM, JANET
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082
; CURRENT FILING DATE: 1999-10-22
; EARLIER APPLICATION NUMBER: 60/105,371
; EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SPO MIMETIC
; US-09-428-082-1025

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 5e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47
US-09-428-082B-87
; Sequence 87, Application US/09428082B
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
```

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: GENERAL INFORMATION:
: APPLICANT: FEIGE, ULRICH
: APPLICANT: LIU, CHUAN-FA
: APPLICANT: CHEETHAM, JANET C.
: APPLICANT: BOONE, THOMAS CHARLES
: TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
: FILE REFERENCE: A-527

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Search completed: November 5, 2003, 19:10:55
Job time : 173 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:05:59 ; Search time 18 Seconds
(without alignments)
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Title: US-09-863-600E-19

Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPQGG 2C

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 248976 seqs, 47010500 residues

Total number of hits satisfying chosen parameters: 248976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents AA.New.*

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4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*

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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	95.1	20	1	PCT-US03-18645-7
2	117	95.1	20	1	PCT-US03-26779-1
3	117	95.1	20	1	PCT-US03-26779-25
4	117	95.1	20	1	PCT-US03-26778-11
5	117	95.1	20	1	PCT-US03-26818-11
6	117	95.1	20	5	US-09-341-590A-117
7	117	95.1	20	6	US-10-651-723-87
8	117	95.1	20	6	US-10-651-723-93
9	117	95.1	20	6	US-10-651-723-1025
10	117	95.1	20	6	US-10-653-048-87
11	117	95.1	20	6	US-10-653-048-93
12	117	95.1	20	6	US-10-653-048-1025
13	117	95.1	20	6	US-10-666-696-87
14	117	95.1	20	6	US-10-666-696-93
15	117	95.1	20	6	US-10-666-696-1025
16	117	95.1	20	7	US-60-485-404-11
17	117	95.1	20	7	US-60-485-404-25
18	117	95.1	22	6	US-10-651-723-97
19	117	95.1	22	6	US-10-653-048-97
20	117	95.1	22	6	US-10-666-696-97
21	117	95.1	23	6	US-10-651-723-94
22	117	95.1	23	6	US-10-651-723-96
23	117	95.1	23	6	US-10-651-723-98
24	117	95.1	23	6	US-10-653-048-94
25	117	95.1	23	6	US-10-653-048-96
26	117	95.1	23	6	US-10-653-048-98
27	117	95.1	27	117	Sequence 7, Appl
28	117	95.1	28	117	Sequence 11, Appl
29	117	95.1	29	117	Sequence 25, Appl
30	117	95.1	30	117	Sequence 11, Appl
31	117	95.1	31	117	Sequence 11, Appl
32	117	95.1	32	117	Sequence 117, Appl
33	117	95.1	33	117	Sequence 87, Appl
34	117	95.1	34	117	Sequence 93, Appl
35	117	95.1	35	117	Sequence 1025, Ap
36	117	95.1	36	117	Sequence 87, Appl
37	117	95.1	37	117	Sequence 93, Appl
38	117	95.1	38	117	Sequence 1025, Ap
39	117	95.1	39	117	Sequence 87, Appl
40	117	95.1	40	117	Sequence 93, Appl
41	117	95.1	41	117	Sequence 1025, Ap
42	117	95.1	42	117	Sequence 11, Appl
43	117	95.1	43	117	Sequence 25, Appl
44	117	95.1	44	117	Sequence 97, Appl
45	117	95.1	45	117	Sequence 97, Appl
46	117	95.1	46	117	Sequence 97, Appl
47	117	95.1	47	117	Sequence 94, Appl
48	117	95.1	48	117	Sequence 96, Appl
49	117	95.1	49	117	Sequence 98, Appl
50	117	95.1	50	117	Sequence 94, Appl
51	117	95.1	51	117	Sequence 96, Appl
52	117	95.1	52	117	Sequence 94, Appl
53	117	95.1	53	117	Sequence 96, Appl
54	117	95.1	54	117	Sequence 98, Appl
55	117	95.1	55	117	Sequence 94, Appl
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58	117	95.1	58	117	Sequence 96, Appl
59	117	95.1	59	117	Sequence 98, Appl
60	117	95.1	60	117	Sequence 94, Appl
61	117	95.1	61	117	Sequence 96, Appl
62	117	95.1	62	117	Sequence 98, Appl
63	117	95.1	63	117	Sequence 94, Appl
64	117	95.1	64	117	Sequence 96, Appl
65	117	95.1	65	117	Sequence 98, Appl
66	105	85.4	18	6	US-10-651-723-425
67	105	85.4	18	6	US-10-651-723-1036
68	105	85.4	18	6	US-10-653-048-425
69	105	85.4	18	6	US-10-653-048-1036
70	105	85.4	18	6	US-10-666-696-425
71	105	85.4	18	6	US-10-666-696-1036
72	100.5	81.7	19	6	US-10-651-723-422
73	100.5	81.7	19	6	US-10-653-048-422
74	100.5	81.7	19	6	US-10-666-696-422
75	95	77.2	26	5	US-09-341-590A-93
76	95	77.2	26	5	US-09-341-590A-94
77	95	77.2	32	5	US-09-341-590A-95
78	89	72.4	20	1	PCT-US03-18645-10
79	89	72.4	20	6	US-10-651-723-90
80	89	72.4	20	6	US-10-651-723-1029
81	89	72.4	20	6	US-10-653-048-90
82	89	72.4	20	6	US-10-653-048-1029
83	89	72.4	20	6	US-10-666-696-90
84	89	72.4	20	6	US-10-666-696-1029
85	85	69.1	20	1	PCT-US03-18645-8
86	85	69.1	20	6	US-10-651-723-88
87	85	69.1	20	6	US-10-651-723-1026
88	85	69.1	20	6	US-10-653-048-88
89	85	69.1	20	6	US-10-653-048-1026
90	85	69.1	20	6	US-10-666-696-88
91	85	69.1	20	6	US-10-666-696-1026
92	81	65.9	20	1	PCT-US03-18645-9
93	81	65.9	20	6	US-10-651-723-89
94	81	65.9	20	6	US-10-651-723-426
95	81	65.9	20	6	US-10-651-723-1030
96	81	65.9	20	6	US-10-651-723-1037
97	81	65.9	20	6	US-10-653-048-89
98	81	65.9	20	6	US-10-653-048-426
99	81	65.9	20	6	US-10-653-048-1030

Sequence 94, Appl
Sequence 96, Appl
Sequence 98, Appl
Sequence 1034, Ap
Sequence 1034, Ap
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Sequence 395, App
Sequence 395, App
Sequence 395, App
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Sequence 92, Appl
Sequence 92, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 95, Appl
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Sequence 339, App
Sequence 340, App
Sequence 339, App
Sequence 340, App
Sequence 417, App
Sequence 417, App
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Sequence 18, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 20, Appl
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Sequence 22, Appl
Sequence 20, Appl
Sequence 425, App
Sequence 1036, Ap
Sequence 422, App
Sequence 422, App
Sequence 422, App
Sequence 93, Appl
Sequence 94, Appl
Sequence 95, Appl
Sequence 10, Appl
Sequence 90, Appl
Sequence 1029, Ap
Sequence 90, Appl
Sequence 1029, Ap
Sequence 8, Appl
Sequence 1026, Ap
Sequence 88, Appl
Sequence 88, Appl
Sequence 1026, Ap
Sequence 88, Appl
Sequence 1026, Ap
Sequence 1026, Ap
Sequence 9, Appl
Sequence 89, Appl
Sequence 426, App
Sequence 1030, App
Sequence 1037, Ap
Sequence 89, Appl
Sequence 426, App
Sequence 1030, App

100 81 65.9 20 6 US-10-653-048-1037 Sequence 1037, Ap

ALIGNMENTS

RESULT 1

PCT-US03-18645-7

; Sequence 7, Application PC/TUS0318645
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Digicayiloglu, Murat
; APPLICANT: Lipton, Stuart A.
; TITLE OF INVENTION: Neuroprotective Synergy of
; FILE REFERENCE: 66821-216
; CURRENT APPLICATION NUMBER: PCT/US03/18645
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,058
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/458,145
; PRIOR FILING DATE: 2003-03-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
PCT-US03-18645-7

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQGG 20

DB 1 GGTYSCHFGLTWVCKPQGG 20

RESULT 2

PCT-US03-26779-11

; Sequence 11, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
PCT-US03-26779-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQGG 20
DB 1 GGTYSCHFGLTWVCKPQGG 20

RESULT 3

PCT-US03-26779-25

; Sequence 25, Application PC/TUS0326779
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeghi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26779
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/485,404
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
PCT-US03-26779-25

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQGG 20

DB 1 GGTYSCHFGLTWVCKPQGG 20

RESULT 4

PCT-US03-26778-11

; Sequence 11, Application PC/TUS0326778
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Sadeghi, Homayoun
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: ORAL DELIVERY OF MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5006-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26778
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/378,094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: EMP1 peptide
; OTHER INFORMATION: 1; Indels 0; Gaps 0;
PCT-US03-26778-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 5
PCT-US03-26818-11
; Sequence 11, Application PC/TUS0326818
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew J.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-WO
; CURRENT APPLICATION NUMBER: PCT/US03/26818
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/378,094
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: EMP1 peptide
PCT-US03-26818-11

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 6
US-09-341-590A-117
; Sequence 117, Application US/09341590A
; GENERAL INFORMATION:
; APPLICANT: LARSEN, BJARNE DUE
; TITLE OF INVENTION: PHARMACOLOGICALLY ACTIVE PEPTIDE CONJUGATES HAVING A
; TITLE REFERENCE: REDUCED TENDENCY TOWARDS ENZYMATIC HYDROLYSIS
; FILE REFERENCE: 55508(45487)
; CURRENT APPLICATION NUMBER: US/09/341,590A
; CURRENT FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: DK 0317/98
; PRIOR FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EMP-1
US-09-341-590A-117

Query Match 95.1%; Score 117; DB 5; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 7

US-10-651-723-87

; Sequence 87, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-87

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 8
US-10-651-723-93
; Sequence 93, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-651-723-93

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 9

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US-10-651-723-1025
; Sequence 1025, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
;
; NAME/KEY: misc feature
; LOCATION: (20)-(20)
; OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-651-723-1025

Query Match          95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 10
US-10-653-048-87
; Sequence 87, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-87

Query Match          95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 11
US-10-653-048-93
; Sequence 93, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 93
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-93

Query Match          95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 12
US-10-653-048-1025
; Sequence 1025, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1025
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-1025

Query Match          95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 13
US-10-666-696-87
; Sequence 87, Application US/10666696
```

GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
APPLICANT: GUDAS, JEAN MARIE
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527A
CURRENT APPLICATION NUMBER: US/10/666,696
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/563,286C
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/428,082
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1157
SOFTWARE: PatentIn version 3.1
SEQ ID NO 87
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-87

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
|||||

RESULT 14
US-10-666-696-93
Sequence 93; Application US/10666696
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
APPLICANT: GUDAS, JEAN MARIE
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527A
CURRENT APPLICATION NUMBER: US/10/666,696
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/563,286C
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/428,082
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1157
SOFTWARE: PatentIn version 3.1
SEQ ID NO 93
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPO-mimetic peptide
FEATURE:
NAME/KEY: misc feature
LOCATION: (20)..(20)
OTHER INFORMATION: Position 20, amino acid linker to an identical sequence
US-10-666-696-93

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGPLTWCKPQGG 20
|||||
RESULT 15
US-10-666-696-1025
Sequence 1025; Application US/10666696
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
APPLICANT: GUDAS, JEAN MARIE
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527A
CURRENT APPLICATION NUMBER: US/10/666,696
CURRENT FILING DATE: 2003-09-19
PRIOR APPLICATION NUMBER: US/09/563,286C
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/428,082
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1157
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1025
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-666-696-1025

Query Match 95.1%; Score 117; DB 6; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20
|||||

RESULT 16
US-60-485-404-11
Sequence 11; Application US/60485404
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homayoun
TITLE OF INVENTION: Transferrin Fusion Protein Libraries
FILE REFERENCE: 054710-5007-PR
CURRENT APPLICATION NUMBER: US/60/485,404
CURRENT FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/406,997
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 10/384,060
PRIOR FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 60/460,829
PRIOR FILING DATE: 2003-04-08
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
OTHER INFORMATION: peptide
US-60-485-404-11

Query Match 95.1%; Score 117; DB 7; Length 20;

```
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 17
US-60-485-404-25
; Sequence 25, Application US/60485404
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; APPLICANT: Turner, Andrew J.
; APPLICANT: Sadeqhi, Homayoun
; TITLE OF INVENTION: Transferrin Fusion Protein Libraries
; FILE REFERENCE: 054710-5007-PR
; CURRENT APPLICATION NUMBER: US/60/485,404
; PRIOR FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/406,997
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 10/384,060
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 60/460,829
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: sequences
US-60-485-404-25

Query Match 95.1%; Score 117; DB 7; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 18
US-10-651-723-97
; Sequence 97, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Position 22 linked through epsilon amine to lysyl, which is li
; OTHER INFORMATION: d to a separate identical sequence through that sequence's alp
US-10-653-048-97

Query Match 95.1%; Score 117; DB 6; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 19
US-10-653-048-97
; Sequence 97, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (22)..(22)
; OTHER INFORMATION: Position 22 linked through epsilon amine to lysyl, which is li
; OTHER INFORMATION: d to a separate identical sequence through that sequence's alp
US-10-653-048-97

Query Match 95.1%; Score 117; DB 6; Length 22;
Best Local Similarity 95.0%; Pred. No. 1.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 20
US-10-666-696-97
; Sequence 97, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
```


; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-94

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 25
US-10-653-048-96
; Sequence 96 Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Position 23, amino acid linker to an identical sequence
US-10-653-048-96

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 26
US-10-653-048-98
; Sequence 98 Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH

; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
; NAME/KEY: misc_feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: At position 23 biotin linked to the sidechain through a linker
US-10-653-048-98

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 27
US-10-666-696-94
; Sequence 94 Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-94

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 28

US-10-666-696-96
; Sequence 96, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: Position 23, amino acid linker to an identical sequence
US-10-666-696-96

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 29
US-10-666-696-98
; Sequence 98, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
; NAME/KEY: misc feature
; LOCATION: (23)..(23)
; OTHER INFORMATION: At position 23 biotin linked to the sidechain through a linker
US-10-666-696-98

Query Match 95.1%; Score 117; DB 6; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
US-10-651-723-1034
; Sequence 1034, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: Fc domain attached at Position 25 of the C-terminus
US-10-651-723-1034

Query Match 95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 31
US-10-653-048-1034
; Sequence 1034, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
US-10-653-048-1034

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)_:..(25)
; OTHER INFORMATION: Pc domain attached at Position 25 of the C-terminus
US-10-653-048-1034

Query Match          95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 32
US-10-666-696-1034
; Sequence 1034, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1034
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Pc domain attached at Position 25 of the C-terminus
US-10-666-696-1034

Query Match          95.1%; Score 117; DB 6; Length 25;
Best Local Similarity 95.0%; Pred. No. 1.9e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 33
US-10-651-723-403
; Sequence 403, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 403
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-FC
US-10-651-723-403

Query Match          95.1%; Score 117; DB 6; Length 36;
Best Local Similarity 95.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 12 GGTYSCHFGPLTWCKPQGG 31

RESULT 34
US-10-653-048-403
; Sequence 403, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 403
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EMP-FC
US-10-653-048-403

Query Match          95.1%; Score 117; DB 6; Length 36;
Best Local Similarity 95.0%; Pred. No. 2.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 12 GGTYSCHFGPLTWCKPQGG 31

RESULT 35
US-10-666-696-403
; Sequence 403, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 40

US-10-653-048-92
; Sequence 92, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 41

US-10-666-696-92
; Sequence 92, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 40

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-92

Query Match 95.1%; Score 117; DB 6; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 42

US-10-651-723-95
; Sequence 95, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-95

Query Match 95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 43

US-10-653-048-95
; Sequence 95, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-653-048-95

Query Match 95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 44

US-10-666-696-95
; Sequence 95, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-mimetic peptide
US-10-666-696-95

Query Match 95.1%; Score 117; DB 6; Length 46;
Best Local Similarity 95.0%; Pred. No. 3.2e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45

US-10-651-723-339
; Sequence 339, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC PEPTIDE
US-10-651-723-339

; OTHER INFORMATION: EPO-MIMETIC
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(11)
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-651-723-339

Query Match 95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 6 GGTYSCHFGPLTWCKPQGG 25

RESULT 46

US-10-651-723-340
; Sequence 340, Application US/10651723
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (49)...(49)
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-651-723-340

Query Match 95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47

US-10-653-048-339
; Sequence 339, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (49)...(49)
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-653-048-339

Query Match 95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

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; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (1)-(1)
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-653-048-339

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 6 GGTYSCHFGLTWCKPQGG 25

RESULT 48
US-10-653-048-340
; Sequence 340, Application US/10653048
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; LOCATION: (49)-(49)
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-653-048-340

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

RESULT 49
US-10-666-696-339
; Sequence 339, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
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; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 339
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 1 of the N-terminus
US-10-666-696-339

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 6 GGTYSCHFGLTWCKPQGG 25

RESULT 50
US-10-666-696-340
; Sequence 340, Application US/10666696
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 340
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EPO-MIMETIC
; NAME/KEY: misc feature
; OTHER INFORMATION: Fc domain attached at Position 49 of the C-terminus
US-10-666-696-340

Query Match          95.1%; Score 117; DB 6; Length 49;
Best Local Similarity 95.0%; Pred. No. 3.4e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGLTWCKPQGG 20

Search completed: November 5, 2003, 19:11:24
Job time : 18 secs
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OM protein - protein search, using sw model

Run on: November 5, 2003, 18:59:48 ; Search time 41 Seconds
(without alignments)
77.428 Million cell updates/sec

Title: US-09-863-600E-19

Perfect score: 123

Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1:07863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	20	AA13641	Erythropoietin rec
2	123	100.0	20	AAU74467	Human erythropoiet
3	119	96.7	20	AA13645	Erythropoietin rec
4	119	96.7	20	AAU74477	Human erythropoiet
5	119	96.7	20	AAU74485	Human erythropoiet
6	117	95.1	20	AAU74478	Erythropoietin rec
7	117	95.1	20	AAU74480	Erythropoietin rec
8	117	95.1	20	AAU74481	Erythropoietin rec
9	117	95.1	20	AAU74482	Erythropoietin rec

10	117	95.1	20	18	AAU26399	Erythropoietin rec
11	117	95.1	20	18	AAU26372	Erythropoietin rec
12	117	95.1	20	18	AAU13646	Erythropoietin rec
13	117	95.1	20	18	AAU13683	Erythropoietin rec
14	117	95.1	20	18	AAU43020	Peptide mimetic of
15	117	95.1	20	18	AAU26963	Monomer subunit of
16	117	95.1	20	18	AAU26975	Monomer subunit of
17	117	95.1	20	18	AAU26997	Monomer subunit of
18	117	95.1	20	21	AAU13501	Erythropoietin der
19	117	95.1	20	21	AAU17031	EPO-mimetic peptid
20	117	95.1	20	21	AAU17921	EPO-mimetic peptid
21	117	95.1	20	22	AAU63738	Peptide agonist fo
22	117	95.1	20	22	AAU97489	Erythropoietin cyc
23	117	95.1	20	22	AAU97492	Erythropoietin cyc
24	117	95.1	20	23	AAU74456	Human erythropoiet
25	117	95.1	20	23	AAU74478	Human erythropoiet
26	117	95.1	20	23	AAU74486	Human erythropoiet
27	117	95.1	20	23	AAU72814	Erythropoietin (EP
28	117	95.1	20	23	AAU72840	Erythropoietin (EP
29	117	95.1	20	23	AAU57650	Erythropoietin rec
30	117	95.1	22	18	AAU13638	Erythropoietin rec
31	117	95.1	22	21	AAU17041	EPO-mimetic peptid
32	117	95.1	22	23	AAU72824	Erythropoietin (EP
33	117	95.1	23	18	AAU26551	Erythropoietin rec
34	117	95.1	23	21	AAU17038	EPO-mimetic peptid
35	117	95.1	23	21	AAU17042	EPO-mimetic peptid
36	117	95.1	23	23	AAU72821	Erythropoietin (EP
37	117	95.1	24	23	AAU72825	Erythropoietin (EP
38	117	95.1	25	23	AAU73394	EPO-mimetic peptid
39	117	95.1	26	21	AAU17930	EPO-mimetic peptid
40	117	95.1	36	21	AAU17313	EMP-Fc fusion cons
41	117	95.1	36	23	AAU73407	EPO mimetic peptid
42	117	95.1	39	21	AAU17312	FC-EMP fusion cons
43	117	95.1	39	23	AAU73406	EPO mimetic peptid
44	117	95.1	40	21	AAU17036	EPO-mimetic peptid
45	117	95.1	40	23	AAU72819	Erythropoietin (EP
46	117	95.1	41	21	AAU17037	EPO-mimetic peptid
47	117	95.1	41	23	AAU72820	Erythropoietin (EP
48	117	95.1	42	20	AAU49902	Erythropoietin rec
49	117	95.1	46	21	AAU17039	EPO-mimetic peptid
50	117	95.1	46	23	AAU72822	Erythropoietin (EP
51	117	95.1	47	21	AAU17040	EPO-mimetic peptid
52	117	95.1	47	23	AAU72823	Erythropoietin (EP
53	117	95.1	49	23	AAU73392	EPO-mimetic peptid
54	117	95.1	49	23	AAU73393	EPO-mimetic peptid
55	117	95.1	50	21	AAU17283	EPO-mimetic peptid
56	117	95.1	51	21	AAU17284	EMP-EMP-Fc fusion
57	117	95.1	57	21	AAU17314	EMP-EMP gene const
58	117	95.1	57	23	AAU73408	FC-EMP protein seq
59	117	95.1	253	21	AAU16964	EMP-Fc protein seq
60	117	95.1	253	21	AAU16965	FC-EPO mimetic pep
61	117	95.1	253	23	AAU73415	EPO mimetic peptid
62	117	95.1	277	21	AAU16966	EMP-EMP-Fc protein
63	117	95.1	277	21	AAU16967	FC-EMP-EMP protein
64	117	95.1	277	21	AAU16967	FC-EMP-EMP nucleic
65	117	95.1	277	23	AAU73418	EMP-EMP-Fc amino a
66	117	95.1	278	23	AAU73417	Human erythropoiet
67	112	91.1	20	18	AAU13648	Erythropoietin rec
68	112	91.1	20	18	AAU13650	Human erythropoiet
69	112	91.1	20	23	AAU74480	Human erythropoiet
70	112	91.1	20	23	AAU74481	Erythropoietin cyc
71	111	90.2	20	18	AAU13625	Erythropoietin rec
72	111	90.2	20	18	AAU13649	Erythropoietin rec
73	111	90.2	20	23	AAU74468	Human erythropoiet
74	109	88.6	20	18	AAU13647	Erythropoietin rec
75	109	88.6	20	23	AAU74479	Human erythropoiet
76	109	88.6	20	23	AAU74484	Human erythropoiet
77	108.5	88.2	22	22	AAU97497	Erythropoietin cyc
78	107	87.0	20	18	AAU13652	Erythropoietin rec
79	107	87.0	20	18	AAU13659	Erythropoietin rec
80	107	87.0	20	23	AAU74483	Human erythropoiet
81	105	85.4	18	18	AAU13626	Erythropoietin rec
82	105	85.4	18	18	AAU13633	Erythropoietin rec

83 105 85.4 18 18 AAY13657 Erythropoietin rec
 84 105 85.4 18 18 AAW26968 Monomer subunit of
 85 105 85.4 18 21 AAB13506 Erythropoietin der
 86 105 85.4 18 21 AAB17321 EPO-mimetic peptid
 87 105 85.4 18 21 AAB17932 EPO-mimetic peptid
 88 105 85.4 18 22 AAB97494 Erythropoietin cyc
 89 105 85.4 18 23 AAU74461 Human erythropoiet
 90 105 85.4 18 23 AAU74470 Human erythropoiet
 91 105 85.4 18 23 ABB72830 Erythropoietin (EP
 92 105 85.4 18 23 ABB72845 Erythropoietin (EP
 93 103 83.7 20 18 AAY13651 Erythropoietin rec
 94 103 83.7 20 23 AAU74482 Human erythropoiet
 95 102 82.9 20 22 AAU05325 R1 and R2 peptide
 96 101 82.1 20 22 AAU05326 R1 and R2 peptide
 97 100.5 81.7 19 21 AAB17318 EPO-mimetic peptid
 98 100.5 81.7 19 23 ABB72827 Erythropoietin (EP
 99 99 80.5 20 22 AAU05307 R1 and R2 peptide
 100 99 80.5 20 22 AAU05315 R1 and R2 peptide

ALIGNMENTS

RESULT 1
 AAY13641
 ID AAY13641 standard; peptide; 20 AA.
 XX
 AC AAY13641;

DT 06-SEP-1999 (first entry)

XX Erythropoietin receptor (EPO-R) binding peptide.

DE
 XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09810.

XX 07-JUN-1995; 95US-0484635.

XX 07-JUN-1995; 95US-0484631.

XX 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX (JOHN) JOHNSON & JOHNSON CORP.

XX (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating

XX disorders characterised by deficiency of EPO, or low or defective

XX red blood cell population

XX Claim 6; Page 68; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which

XX binds to erythropoietin (EPO) receptor and which includes the amino acid

XX sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trip-Xaa4-Cys, where Xaa1 = Arg,

CC end stage renal failure or dialysis; anaemia associated with AIDS;
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
 CC specific examples of EPO-R binding peptides.

XX Sequence 20 AA;

SQ Query Match 100.0%; Score 123; DB 18; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.7e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

DB 1 GGTASCHFGPLTWCKPQGG 20

RESULT 2

AAU74467

ID AAU74467 standard; Peptide; 20 AA.

XX AC AAU74467;

XX DT 09-APR-2002 (first entry)

XX Human erythropoietin neuroprotective peptide EMP-6.

DE
 XX Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
 KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
 KW neurological damage; neurodegenerative disorder; neurological disorder;
 KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-6;
 KW human immunodeficiency virus; haematology; autoimmune disease;
 KW inflammatory disorder; infectious disease.

XX Homo sapiens.

XX WO200191780-A1.

XX 06-DEC-2001.

XX 23-MAY-2001; 2001WO-US16654.

XX 26-MAY-2000; 2000US-207654P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
 XX Johnson DL;

XX WPI; 2002-114307/15.

XX Treating patients having condition mediated by neurotoxicity,
 PT neurodegeneration or neurological damage, involves administering to
 PT patient a peptide comprising monomeric peptides that bind to
 PT erythropoietin receptor

XX Claim 14; Page 40; 75pp; English.

XX The invention relates to a method for treating a patient with a condition
 CC mediated by neurotoxicity, neurodegeneration or neurological damage,
 CC involving administering a peptide comprising one or more monomeric
 CC peptides that bind to the human erythropoietin (EPO) receptor. The method
 CC is useful for treating acute and chronic neurodegenerative disorders
 CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
 CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
 CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
 CC La Tourette's disease, Tay-Sachs disease, and prion diseases including
 CC Creutzfeldt-Jakob and kuru, neurological and psychiatric manifestations
 CC associated with peripheral diseases including blood loss of any kind,
 CC renal failure, conditions associated with anaemia, and neurological and

CC neuropsychiatric manifestations including haematological and
 CC non-haematological malignancies/cancer, symptoms or complications in
 CC patients receiving chemotherapy, inflammatory and infectious disorders
 CC such as human immunodeficiency viral infections, and chronic systemic
 CC autoimmune diseases such as systemic lupus erythematosus. The method is
 CC also useful for prevention of plexopathies and neuropathies. This
 CC sequence represents a human erythropoietin neuroprotective peptide of the
 CC invention.

XX
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 123; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 4.7e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
 |||||
 Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3

AAU13645
 ID AAY13645 standard; peptide; 20 AA.

AC AAY13645;

XX
 DT 06-SEP-1999 (first entry)

XX Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09810.

XX 07-JUN-1995; 95US-0484635.

XX 07-JUN-1995; 95US-0484631.

XX 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX (JOHJ) JOHNSON & JOHNSON CORP.

XX (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating

XX disorders characterised by deficiency of EPO, or low or defective

XX red blood cell population

XX Claim 6; Page 68; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO
 CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS,
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal

CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
 XX specific examples of EPO-R binding peptides.

SQ Sequence 20 AA;

Query Match 96.7%; Score 119; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. NO. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
 |||||
 Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4

AAU74477
 ID AAU74477 standard; Peptide; 20 AA.

AC AAU74477;

XX
 DT 09-APR-2002 (first entry)

XX Human erythropoietin neuroprotective peptide EMP-7.

XX Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
 KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
 KW neurological damage; neurodegenerative disorder; neurological disorder;
 KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
 KW human immunodeficiency virus; haematology; autoimmune disease;
 KW inflammatory disorder; infectious disease; EMP-7.

OS Homo sapiens.

XX WO200191780-A1.

XX 06-DEC-2001.

XX 23-MAY-2001; 2001WO-US16654.

XX 26-MAY-2000; 2000US-207654P.

XX (ORTH) ORTHO-MCNEIL PHARM INC.

XX Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
 XX Johnson DU;

XX WPI; 2002-114307/15.

XX Treating patients having condition mediated by neurotoxicity,
 PT neurodegeneration or neurological damage, involves administering to
 PT patient a peptide comprising monomeric peptides that bind to
 PT erythropoietin receptor

XX Claim 14; Page 41; 75pp; English.

XX The invention relates to a method for treating a patient with a condition
 CC mediated by neurotoxicity, neurodegeneration or neurological damage,
 CC involving administering a peptide comprising one or more monomeric
 CC peptides that bind to the human erythropoietin (EPO) receptor. The method
 CC is useful for treating acute and chronic neurodegenerative disorders
 CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
 CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
 CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
 CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
 CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
 CC associated with peripheral diseases including blood loss of any kind,
 CC renal failure, conditions associated with anaemia, and neurological and
 CC neuropsychiatric manifestations including haematological and
 CC non-haematological malignancies/cancer, symptoms or complications in
 CC patients receiving chemotherapy, inflammatory and infectious disorders

CC such as human immunodeficiency viral infections, and chronic systemic
 CC autoimmune diseases such as systemic lupus erythematosus. The method is
 CC also useful for prevention of plexopathies and neuropathies. This
 CC sequence represents a human erythropoietin neuroprotective peptide of the
 CC invention.

XX
 XX
 SQ Sequence 20 AA;
 Query Match 96.7%; Score 119; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 5
 AAU74485
 ID AAU74485 standard; Peptide; 20 AA.

XX
 AC AAU74485;
 DT 09-APR-2002 (first entry)
 XX
 DE Human erythropoietin neuroprotective generic peptide (EMP-28-EMP-33).
 XX
 KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
 KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
 KW neurological damage; neurodegenerative disorder; neurological disorder;
 KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-32;
 KW human immunodeficiency virus; haematology; autoimmune disease; EMP-31;
 KW inflammatory disorder; infectious disease; EMP-28; EMP-29; EMP-30;
 KW EMP-33.
 XX
 XX Homo sapiens.

XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 4
 FT /note= "D-Tyr (EMP-28), p-NO 2-Phe (EMP-29), p-NH 2-Phe
 FT (EMP-30), p-F-Phe (EMP-31), p-I-Phe (EMP-32) or
 FT 3,5-dibromo-Tyr (EMP-33)"
 VV

PN WO200191780-A1.
 XX
 PD 06-DEC-2001.
 XX
 XX 23-MAY-2001; 2001WO-US16654.
 XX
 XX 26-MAY-2000; 2000US-207654P.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX
 XX Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
 PI Johnson DL;
 XX
 XX WPI; 2002-114307/15.

XX
 XX
 PT Treating patients having condition mediated by neurotoxicity,
 PT neurodegeneration or neurological damage, involves administering to
 PT patient a peptide comprising monomeric peptides that bind to
 PT erythropoietin receptor -
 XX
 XX
 PS Claim 14; Page 41; 75pp; English.

XX
 CC The invention relates to a method for treating a patient with a condition
 CC mediated by neurotoxicity, neurodegeneration or neurological damage,
 CC involving administering a peptide comprising one or more monomeric
 CC peptides that bind to the human erythropoietin (EPO) receptor. The method
 CC is useful for treating acute and chronic neurodegenerative disorders
 CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
 CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
 CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De

CC La Tourette's disease, Tay-Sach's disease, and prion diseases including
 CC Creutzfeldt-Jakob and Kuru neurological and psychiatric manifestations
 CC associated with peripheral diseases including blood loss of any kind,
 CC renal failure, conditions associated with anaemia, and neurological and
 CC neuropsychiatric manifestations including haematological and
 CC non-haematological malignancies/cancer, symptoms or complications in
 CC patients receiving chemotherapy, inflammatory and infectious disorders
 CC such as human immunodeficiency viral infections, and chronic systemic
 CC autoimmune diseases such as systemic lupus erythematosus. The method is
 CC also useful for prevention of plexopathies and neuropathies. This
 CC sequence represents a human erythropoietin neuroprotective peptide of the
 CC invention.

XX
 XX
 SQ Sequence 20 AA;
 Query Match 96.7%; Score 119; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 1.6e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 6
 AAU26550
 ID AAU26550 standard; peptide; 20 AA.

XX
 AC AAU26550;
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX
 OS Synthetic.
 XX
 XX WO9640749-A1.

PN 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US09810.

XX
 XX 07-JUN-1995; 95US-0484635.
 PR 07-JUN-1995; 95US-0484631.
 PR 19-NOV-1993; 93US-0155940.

XX
 XX (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PA (JOHJ) JOHNSON & JOHNSON CORP.
 PA (ORTH) ORTHO PHARM CORP.

XX
 XX Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
 PI Mulcahy L, Wrighton NC;
 XX

XX
 XX WPI; 1997-052225/05.

XX
 XX Erythropoietin receptor binding peptide - useful for treating
 PT disorders characterised by deficiency of EPO, or low or defective
 PT red blood cell population

XX
 PS Disclosure; Page 28; 95pp; English.

XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trip-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO

CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS;
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
 CC representative peptides falling within the above peptide motif and
 CC isolated during the affinity selection process.

XX Sequence 20 AA;
 SQ Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 7
 AAY26481
 ID AAY26481 standard; peptide; 20 AA.

XX AC AAY26481;
 XX DT 06-SEP-1999 (first entry)

XX Erythropoietin receptor (EPO-R) binding peptide.

DE Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09810.

XX PR 07-JUN-1995; 95US-0484635.

XX PR 07-JUN-1995; 95US-0484631.

XX PR 19-NOV-1993; 93US-0155940.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PA (JOHJ) JOHNSON & JOHNSON CORP.

XX PA (ORTH) ORTHO PHARM CORP.

XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX PI Mulcahy L, Wrighton NC;

XX DR WPI; 1997-052225/05.

XX PT Erythropoietin receptor binding peptide - useful for treating

XX disorders characterised by deficiency of EPO, or low or defective

XX red blood cell population

XX PS Disclosure; Page 23; 95pp; English.

XX CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO
 CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS;

CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
 CC representative peptides falling within the above peptide motif and
 CC isolated during the affinity selection process.

XX Sequence 20 AA;

SQ Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 8
 AAY26406
 ID AAY26406 standard; peptide; 20 AA.

XX AC AAY26406;

XX DT 06-SEP-1999 (first entry)

XX Erythropoietin receptor (EPO-R) binding peptide.

DE Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09810.

XX PR 07-JUN-1995; 95US-0484635.

XX PR 07-JUN-1995; 95US-0484631.

XX PR 19-NOV-1993; 93US-0155940.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PA (JOHJ) JOHNSON & JOHNSON CORP.

XX PA (ORTH) ORTHO PHARM CORP.

XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX PI Mulcahy L, Wrighton NC;

XX DR WPI; 1997-052225/05.

XX PT Erythropoietin receptor binding peptide - useful for treating

XX disorders characterised by deficiency of EPO, or low or defective

XX red blood cell population

XX PS Disclosure; Page 19; 95pp; English.

XX CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO
 CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS;
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal

CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

XX
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.le-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 9
AAY26387
ID AAY26387 standard; peptide; 20 AA.

XX
XX
AC AAY26387;

DT 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

PN 19-DEC-1996.

PD 07-JUN-1996; 96WO-US09810.

PF 07-JUN-1995; 95US-0484635.

PR 07-JUN-1995; 95US-0484631.

PR 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (JOHJ) JOHNSON & JOHNSON CORP.

PA (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LX, Kashyap AK;

PI Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating

PT disorders characterised by deficiency of EPO, or low or defective

PT red blood cell population

XX Disclosure; Page 17; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia, cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as

CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
CC representative peptides falling within the above peptide motif and
CC isolated during the affinity selection process.

XX
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.le-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 10

AAY26399

ID AAY26399 standard; peptide; 20 AA.

XX
XX
AC AAY26399;

DT 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

OS Synthetic.

XX WO9640749-A1.

PN 19-DEC-1996.

PD 07-JUN-1996; 96WO-US09810.

PF 07-JUN-1995; 95US-0484635.

PR 07-JUN-1995; 95US-0484631.

PR 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (JOHJ) JOHNSON & JOHNSON CORP.

PA (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LX, Kashyap AK;

PI Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating

PT disorders characterised by deficiency of EPO, or low or defective

PT red blood cell population

XX Disclosure; Page 18; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO
CC or a low or defective red blood cell population. It can be used to treat
CC end stage renal failure or dialysis; anaemia associated with AIDS,
CC autoimmune disease, chronic inflammatory diseases or malignancy;
CC beta-thalassaemia, cystic fibrosis; early anaemia of prematurity; spinal
CC cord injury; acute blood loss; aging; and neoplastic disease states
CC accompanied by abnormal erythropoiesis. The peptides can also be used as
CC reagents for detecting EPO receptors on living cells, in biological
CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are

CC representative peptides falling within the above peptide motif and
 CC isolated during the affinity selection process.

SQ Sequence 20 AA;
 Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.le-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 11
 AAY26372
 ID AAY26372 standard; peptide; 20 AA.
 XX
 AC AAY26372;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 XX
 PN WO9640749-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09810.
 XX
 PR 07-JUN-1995; 95US-0484635.
 PR 07-JUN-1995; 95US-0484631.
 PR 19-NOV-1993; 93US-0155940.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PA (JOHJ) JOHNSON & JOHNSON CORP.
 PA (ORTH) ORTHO PHARM CORP.
 XX
 PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
 PI Mulcahy L, Wrighton NC;
 XX
 WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating
 PT disorders characterised by deficiency of EPO, or low or defective
 PT red blood cell population

PS Disclosure; Page 16; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO
 CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS,
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY26352-548 are
 CC representative peptides falling within the above peptide motif and
 CC isolated during the affinity selection process.

XX
 SQ Sequence 20 AA;
 Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.le-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 12
 AAY13646
 ID AAY13646 standard; peptide; 20 AA.
 XX
 AC AAY13646;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 XX
 PN WO9640749-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09810.
 XX
 PR 07-JUN-1995; 95US-0484635.
 PR 07-JUN-1995; 95US-0484631.
 PR 19-NOV-1993; 93US-0155940.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PA (JOHJ) JOHNSON & JOHNSON CORP.
 PA (ORTH) ORTHO PHARM CORP.
 XX
 PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;
 PI Mulcahy L, Wrighton NC;
 XX
 WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating
 PT disorders characterised by deficiency of EPO, or low or defective
 PT red blood cell population

PS Claim 6; Page 68; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO
 CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anaemia associated with AIDS,
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAY13624-661 represent
 CC specific examples of EPO-R binding peptides.

XX Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 13

AAV13683
ID AAY13683 standard; peptide; 20 AA.

XX AC AAY13683;

XX DT 06-SEP-1999 (first entry)

XX DE Erythropoietin receptor (EPO-R) binding peptide.

XX KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
XX KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
XX KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
XX KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX OS Synthetic.

XX XX WO9640749-A1.

XX PD 19-DEC-1996.

XX PP 07-JUN-1996; 96WO-US09810.

XX PR 07-JUN-1995; 95US-0484635.

XX PR 07-JUN-1995; 95US-0484631.

XX PR 19-NOV-1993; 93US-0155940.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PA (JOHJ) JOHNSON & JOHNSON CORP.

XX PA (ORTH) ORTHO PHARM CORP.

XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX PI Mulcahy L, Wrighton NC;

XX XX WPI; 1997-052225/95.

XX PT Erythropoietin receptor binding peptide - useful for treating

XX PT disorders characterised by deficiency of EPO, or low or defective

XX PT red blood cell population

XX PS Disclosure; Fig 2; 95pp; English.

XX CC The invention describes a peptide of 10-40 amino acid residues which
XX CC binds to erythropoietin (EPO) receptor and which includes the amino acid
XX CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
XX CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
XX CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
XX CC the peptide may be cyclised or dimethylated. The peptide can be used to
XX CC treat a patient having a disorder characterised by a deficiency of EPO
XX CC or a low or defective red blood cell population. It can be used to treat
XX CC end stage renal failure or dialysis; anaemia associated with AIDS,
XX CC autoimmune disease, chronic inflammatory diseases or malignancy;
XX CC beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal
XX CC cord injury; acute blood loss; aging; and neoplastic disease states
XX CC accompanied by abnormal erythropoiesis. The peptides can also be used as
XX CC reagents for detecting EPO receptors on living cells, in biological
XX CC fluids, in tissue homogenates, etc. Sequences AAY13662-735 are
XX CC representative peptides of the invention.

XX SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 14

AAW43020
ID AAW43020 standard; peptide; 20 AA.

XX AC AAW43020;

XX DT 05-MAY-1998 (first entry)

XX DE Peptide mimetic of erythropoietin.

XX KW EMP1; peptide mimetic; erythropoietin; EPO; mimic; EPO-receptor;
XX KW 3-dimensional co-ordinate; atom subset; extracellular domain;
XX KW criteria data set; CDS; agonist; EPO activity; treatment; anaemia.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Disulfide-bond 6..15

XX PN WO9741526-A1.

XX XX 06-NOV-1997.

XX PF 28-APR-1997; 97WO-US07218.

XX PR 26-APR-1996; 96US-0641071.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Johnson DL, Jolliffe LK, Livnah O, Stura EA, Wilson IA;

XX DR WPI; 1997-549970/50.

XX PT Identifying potential mimics of erythropoietin for treating anaemia
XX PT - using computer analysis of coordinates of the complex of
XX PT erythropoietin receptor domain with a known peptide mimic

XX PS Claim 1; Page 79; 85pp; English.

XX CC The present peptide, EMP1, is a peptide mimetic of erythropoietin (EPO).
XX CC EPO is the primary regulator of proliferation and differentiation of
XX CC immature erythroid cells. EMP1 competes with EPO in receptor binding
XX CC assays, and induces cellular proliferation of cell lines engineered to
XX CC be responsive to EPO. Further, EMP1 demonstrates significant
XX CC erythropoietic effects in mice. The sequence of EMP1 is unrelated to EPO.
XX CC Potential mimics of EPO are identified by supplying a computer with
XX CC 3-dimensional co-ordinates of a subset of atoms in EMP1 when this has
XX CC been co-crystallised with the 1-225 amino acid fragment (the
XX CC extracellular domain) of the EPO-receptor, to generate a criteria data
XX CC set (CDS). The computer then compares the CDS with a database of chemical
XX CC structures and those structures with a portion structurally similar to
XX CC CDS are selected and displayed. Alternatively, the computer constructs a
XX CC model of a chemical structure having a portion structurally similar to
XX CC CDS and displays it. The EPO mimics are agonists of the EPO-receptor in
XX CC vivo or in vitro tests of EPO activity. They are potentially useful in
XX CC the treatment of anaemia caused by chronic renal failure, cancer
XX CC chemotherapy or treatment with azidothymidine.

XX SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 18; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 15
 AAW26975
 ID AAW26963 standard; peptide; 20 AA.
 AC AAW26963;
 DT 10-NOV-1997 (first entry)
 DE Monomer subunit of erythropoietin receptor binding dimer.
 KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
 KW treatment; disorder; deficiency; low; defective; red blood cell;
 KW erythrocyte; population; cell surface; agonist; end stage; renal;
 KW failure; dialysis; anaemia; anemia; AIDS; chronic;
 KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
 KW autoimmune; transfusion.
 OS Synthetic.
 XX WO9640772-A2.
 XX 19-DEC-1996.
 XX 06-JUN-1996; 96WO-US09469.
 XX 07-JUN-1995; 95US-0484135.
 XX (ORTH) ORTHO PHARM CORP.
 XX (JOHJ) JOHNSON & JOHNSON.
 XX Johnson DL, Zivin RA;
 PI WPI; 1997-099920/09.
 DR Activating cell surface receptors using peptide dimer agonists -
 PT also, new dimers of erythropoietin receptor binding peptide(s)
 PT useful for treating patient having disorder characterised by EPO
 PT deficiency
 XX Claim 6; Page 93; 110pp; English.
 XX The present peptide is a monomer subunit of an erythropoietin (EPO)
 CC receptor binding dimer, which comprises 2 EPO receptor binding
 CC monomers of 10 to 40 amino acids, and activates or improves the
 CC bioactivity of the EPO cell surface receptor. The dimer can be used
 CC to treat disorders resulting from EPO deficiency by improving the
 CC activity of its cell surface receptor, e.g. end stage renal
 CC failure/dialysis, anaemia associated with AIDS or chronic
 CC inflammatory diseases such as rheumatoid arthritis and chronic
 CC bowel inflammation and autoimmune disease. It can also be used to
 CC boost the red cell count of a patient prior to surgery or as
 CC pretreatment to transfusion. The dimer peptide exhibits increased
 CC biological potency in vitro and in vivo relative to its component
 CC monomeric agonists. Dimerisation may also convert cell surface
 CC receptor antagonists into agonists.
 XX Sequence 20 AA;
 SQ
 Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 16
 AAW26975
 ID AAW26975 standard; peptide; 20 AA.
 XX

AC AAW26975;
 XX 11-NOV-1997 (first entry)
 DE Monomer subunit of erythropoietin receptor binding dimer.
 KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
 KW treatment; disorder; deficiency; low; defective; red blood cell;
 KW erythrocyte; population; cell surface; agonist; end stage; renal;
 KW failure; dialysis; anaemia; anemia; AIDS; chronic;
 KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
 KW autoimmune; transfusion.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acylated"
 FT WO9640772-A2.
 XX 19-DEC-1996.
 XX 06-JUN-1996; 96WO-US09469.
 XX 07-JUN-1995; 95US-0484135.
 XX (ORTH) ORTHO PHARM CORP.
 XX (JOHJ) JOHNSON & JOHNSON.
 XX Johnson DL, Zivin RA;
 PI WPI; 1997-099920/09.
 DR Activating cell surface receptors using peptide dimer agonists -
 PT also, new dimers of erythropoietin receptor binding peptide(s)
 PT useful for treating patient having disorder characterised by EPO
 PT deficiency
 XX Example 5; Fig 9; 110pp; English.
 XX The present peptide is a specific example of a claimed generic
 CC monomer subunit of an erythropoietin (EPO) receptor binding dimer,
 CC which comprises 2 EPO receptor binding monomers of 10 to 40 amino
 CC acids, and activates or improves the bioactivity of the EPO cell
 CC surface receptor. The dimer can be used to treat disorders
 CC resulting from EPO deficiency by improving the activity of its
 CC cell surface receptor, e.g. end stage renal failure/dialysis,
 CC anaemia associated with AIDS or chronic inflammatory diseases such
 CC as rheumatoid arthritis and chronic bowel inflammation and
 CC autoimmune disease. It can also be used to boost the red cell
 CC count of a patient prior to surgery or as pretreatment to
 CC transfusion. The dimer peptide exhibits increased biological
 CC potency in vitro and in vivo relative to its component monomeric
 CC agonists. Dimerisation may also convert cell surface receptor
 CC antagonists into agonists.
 XX Sequence 20 AA;
 SQ
 Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 17
 AAW26997
 ID AAW26997 standard; peptide; 20 AA.
 XX AAW26997;
 AC

XX 11-NOV-1997 (first entry)
 XX Monomer subunit of erythropoietin receptor binding dimer.
 DE
 XX
 XX Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
 KW treatment; disorder; deficiency; low; defective; red blood cell;
 KW erythrocyte; population; cell surface; agonist; end stage; renal;
 KW failure; dialysis; anaemia; anemia; AIDS; chronic;
 KW inflammatory; disease; rheumatoid arthritis; bowel inflammation;
 KW autoimmune; transfusion.
 XX
 XX Synthetic.
 OS
 XX WO9640772-A2.
 PN
 XX 19-DEC-1996.
 PD
 XX 06-JUN-1996; 96WO-US09469.
 PF
 XX 07-JUN-1995; 95US-0484135.-
 PR
 XX (ORTH) ORTHO PHARM CORP.
 PA (JOHN) JOHNSON & JOHNSON.
 PA
 XX Johnson DL, Zivin RA;
 PI
 XX WPI; 1997-099920/09.
 DR
 XX Activating cell surface receptors using peptide dimer agonists -
 XX also, new dimers of erythropoietin receptor binding peptide(s)
 PT useful for treating patient having disorder characterised by EPO
 PT deficiency
 PT
 XX Disclosure; Fig 9; 110pp; English.
 PS
 XX The present peptide is a specific example of a claimed generic
 CC monomer subunit of an erythropoietin (EPO) receptor binding dimer,
 CC which comprises 2 EPO receptor binding monomers of 10 to 40 amino
 CC acids, and activates or improves the bioactivity of the EPO cell
 CC surface receptor. The dimer can be used to treat disorders
 CC resulting from EPO deficiency by improving the activity of its
 CC cell surface receptor, e.g. end stage renal failure/dialysis,
 CC anaemia associated with AIDS or chronic inflammatory diseases such
 CC as rheumatoid arthritis and chronic bowel inflammation and
 CC autoimmune disease. It can also be used to boost the red cell
 CC count of a patient prior to surgery or as pretreatment to
 CC transfusion. The dimer peptide exhibits increased biological
 CC potency in vitro and in vivo relative to its component monomeric
 CC agonists. Dimerisation may also convert cell surface receptor
 CC antagonists into agonists.
 CC
 XX Sequence 20 AA;
 SQ
 Query Match 95.1%; Score 117; DB 18; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 18
 AAB13501
 ID AAB13501 standard; peptide; 20 AA.
 XX
 AC AAB13501;
 XX
 XX 02-NOV-2000 (first entry)
 DT
 XX Erythropoietin derived peptide #2.
 DE
 XX

KW Erythropoietin derivative; diagnostic agent; therapeutic agent.
 XX Unidentified.
 OS
 XX US6077939-A.
 PN
 XX 20-JUN-2000.
 PD
 XX 04-AUG-1997; 97US-0905310.
 PF
 XX 04-AUG-1997; 97US-0905310.
 PR
 XX (ORTH) ORTHO-MCNEIL PHARM. INC.
 PA
 XX Wei Z, Ghosh-Dastidar P, Menon-Rudolph S;
 PI WPI; 2000-450981/39.
 PN
 XX Covalently binding a water-soluble polymer to the N-terminal
 PT alpha-carbon atom of a polypeptide for producing therapeutic and
 PT diagnostic agents, by contacting the transaminated polypeptide with the
 PT polymer to form a hydrazone bond
 PT
 XX Disclosure; Column 5; 21pp; English.
 PS
 XX The present sequence is a peptide derivative of erythropoietin. It can be
 CC used in the method of the invention, which involves the production of
 CC compositions comprising a polypeptide with a water soluble polymer
 CC covalently bound to the N-terminal alpha carbon by a hydrazone or an
 CC oxime (or the reduced version of each) bond. This is useful as previous
 CC methods were more time consuming and labour-intensive, as well as being
 CC less precise. The composition can be used to produce diagnostic and
 CC therapeutic agents.
 CC
 XX Sequence 20 AA;
 SQ
 Query Match 95.1%; Score 117; DB 21; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 19
 AAB17031
 ID AAB17031 standard; Peptide; 20 AA.
 XX
 AC AAB17031;
 XX
 XX 31-OCT-2000 (first entry)
 DT
 XX EPO-mimetic peptide sequence SEQ ID NO:87.
 DE
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 KW
 XX Synthetic.
 OS
 XX WO200024782-A2.
 PN
 XX 04-MAY-2000.
 PD
 XX 25-OCT-1999; 99WO-US25044.
 PF
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 PR

XX (AMGE-) AMGEN INC.
 XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX Claim 13; Page 224; 608pp; English.
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX SQ Sequence 20 AA;
 Query Match 95.1%; Score 117; DB 21; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 20
 AAB17921
 ID AAB17921 standard; Peptide; 20 AA.
 XX
 XX AAB17921;
 XX 31-OCT-2000 (first entry)
 XX EPO-mimetic peptide sequence SEQ ID NO:1025.
 DE Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 XX Synthetic.
 XX WO200024782-A2.
 PN 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US25044.
 XX 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX (AMGE-) AMGEN INC.
 PA

XX Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX Claim 13; Page 556; 608pp; English.
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention are
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX
 XX SQ Sequence 20 AA;
 Query Match 95.1%; Score 117; DB 21; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20
 RESULT 21
 AAG63738
 ID AAG63738 standard; peptide; 20 AA.
 XX
 XX AAG63738;
 XX 29-OCT-2001 (first entry)
 XX Peptide agonist for the erythropoietin receptor (EPO-R).
 DE Insulin-like growth factor; IGF; IGF-1; IGF binding protein; IGFBP;
 KW hyperglycemic disorder; obesity-related disorder; neurological disorder;
 KW cardiac disorder; anabolic disorder; renal disorder; neuroprotection;
 KW immunological disorder; kidney regeneration; degenerative disorder;
 KW hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;
 KW metabolic stress; growth hormone deficiency; diabetes; short stature;
 KW osteoporosis; obesity; erythropoietin receptor.
 XX
 XX Unidentified.
 XX US6251865-B1.
 XX 26-JUN-2001.
 XX 31-MAR-1998; 98US-0052888.
 XX 04-APR-1997; 97US-0825852.
 XX (GETH) GENENTECH INC.
 XX Clark RG, Lowman HB, Robinson ICAF;
 XX

DR WPI: 2001-520042/57.
XX
PT Isolated peptides used to increase serum and tissue levels of
PT insulin-like growth factor in those with hyperglycemic,
PT obesity-related, neurological, cardiac, anabolic, renal or
PT immunological disorders -
XX
XX Example 7; Column 53; 108pp; English.
PS
PS The present sequence is an agonist for the erythropoietin receptor.
XX
XX The specification describes insulin-like growth factor (IGF)-1 agonists,
CC which are used to increase serum and tissue levels of IGF-1 in mammals,
CC with hyperglycemic, obesity-related, neurological, cardiac, anabolic,
CC renal or immunological disorders. They may also be used to increase whole
CC body, bone and muscle growth rate in normal and hypopituitary animals,
CC to protect body weight and nitrogen loss during catabolic states,
CC kidney regeneration, to treat peripheral and central nervous system
CC (CNS) degenerative disorders and promote neuroprotection or repair
CC following CNS damage or injury, to treat hypoxia, to promote wound
CC healing, for cardiac regeneration, to reverse cancer cachexia, to
CC inhibit angiogenesis, to regenerate the gastrointestinal tract, to
CC stimulate mammary function, to counteract IGF-1-dependent actions of
CC growth hormone such as metabolic stress, age-related decline in growth
CC hormone activity and adult growth hormone deficiency, to treat maturity
CC onset diabetes and/or to treat specific IGF deficiency. They may also
CC be used to treat growth-hormone resistant short stature, growth hormone
CC insensitivity syndrome, osteoporosis and catabolic states, and reduce
CC obesity.
XX
XX Sequence 20 AA;
SQ

Query Match 95.1%; Score 117; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20
|||||

RESULT 23
AAB97489
ID AAB97489 standard; peptide; 20 AA.
XX
AC AAB97489;
XX
DT 03-AUG-2001 (first entry);
XX
DE Erythropoietin cyclic mimetic peptide #1.
XX
KW Erythropoietin; mimetic; EPO; cyclic; EPO binding protein; EBP;
XX drug discovery.
XX Synthetic.
XX
XX US6221608-B1.
XX
XX 24-APR-2001.
XX
XX 22-JAN-1997; 97US-0786690.
XX
XX 22-JAN-1997; 97US-0786690.
XX
XX (ORTH) ORTHO PHARM CORP.
XX
XX Middleton SA, Johnson D, McMahon FJ, Mulkahy LS, Jolliffe LK;
XX
XX WPI: 2001-327242/34.
XX
XX Identifying a modulator that dimerises a receptor, useful for
PT identifying and purifying erythropoietin receptor binding proteins -
XX
XX Example 10; Column 31; 30pp; English.
PS
PS The present invention describes a method of identifying a modulator that
CC dimerises a receptor, involving combining a test compound, a preformed
CC dimerisation template and a labeled receptor dimerising ligand, measuring
CC competitive binding of the test compound, adding the modulator to cells
CC which proliferate in response to ligand binding and measuring
CC proliferation of the cells in the presence of the test compound. In
CC particular, this is useful where the preformed dimerisation template is
CC an erythropoietin (EPO) receptor, such as EPO binding protein (EBP). This
CC method is useful in the drug discovery of proteins which bind to EBP.
XX
XX Sequence 20 AA;
SQ

Query Match 95.1%; Score 117; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20
|||||

RESULT 22
AAB97489
ID AAB97489 standard; peptide; 20 AA.
XX
AC AAB97489;
XX
DT 03-AUG-2001 (first entry);
XX
DE Erythropoietin cyclic mimetic peptide #1.
XX
KW Erythropoietin; mimetic; EPO; cyclic; EPO binding protein; EBP;
XX drug discovery.
XX Synthetic.
XX
XX US6221608-B1.
XX
XX 24-APR-2001.
XX
XX 22-JAN-1997; 97US-0786690.
XX
XX 22-JAN-1997; 97US-0786690.
XX
XX (ORTH) ORTHO PHARM CORP.
XX
XX Middleton SA, Johnson D, McMahon FJ, Mulkahy LS, Jolliffe LK;
XX
XX WPI: 2001-327242/34.
XX
XX Identifying a modulator that dimerises a receptor, useful for
PT identifying and purifying erythropoietin receptor binding proteins -
XX
XX Example 10; Column 31; 30pp; English.
PS
PS The present invention describes a method of identifying a modulator that
CC dimerises a receptor, involving combining a test compound, a preformed
CC dimerisation template and a labeled receptor dimerising ligand, measuring
CC competitive binding of the test compound, adding the modulator to cells
CC which proliferate in response to ligand binding and measuring
CC proliferation of the cells in the presence of the test compound. In
CC particular, this is useful where the preformed dimerisation template is
CC an erythropoietin (EPO) receptor, such as EPO binding protein (EBP). This
CC method is useful in the drug discovery of proteins which bind to EBP.
XX
XX Note: This sequence is stated in the specification as being the same as

CC that shown in column 22 of the specification. However, the sequences
CC differ at several positions.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 24
AAU74456
ID AAU74456 standard; Peptide; 20 AA.
XX
AC AAU74456;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-1.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV; EMP-1;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
XX
DR WPI; 2002-114307/15.
XX
PT Treating patients having condition mediated by neurotoxicity.
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 40; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This

CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;

Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 25
AAU74478
ID AAU74478 standard; Peptide; 20 AA.
XX
AC AAU74478;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-8.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease; EMP-8.
XX
OS Homo sapiens.
XX
PN WO200191780-A1.
XX
PD 06-DEC-2001.
XX
PF 23-MAY-2001; 2001WO-US16654.
XX
PR 26-MAY-2000; 2000US-207654P.
XX
PA (ORTH) ORTHO-MCNEIL PHARM INC.
XX
PI Smith-Swintosky V, Renzi M, Plata-Salaman C, Jolliffe L, Farrell F;
PI Johnson DL;
XX
DR WPI; 2002-114307/15.
XX
PT Treating patients having condition mediated by neurotoxicity,
PT neurodegeneration or neurological damage, involves administering to
PT patient a peptide comprising monomeric peptides that bind to
PT erythropoietin receptor -
XX
PS Claim 14; Page 41; 75pp; English.
XX
CC The invention relates to a method for treating a patient with a condition
CC mediated by neurotoxicity, neurodegeneration or neurological damage,
CC involving administering a peptide comprising one or more monomeric
CC peptides that bind to the human erythropoietin (EPO) receptor. The method
CC is useful for treating acute and chronic neurodegenerative disorders
CC including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
CC disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
CC lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
CC La Tourette's disease, Tay-Sachs's disease, and prion diseases including
CC Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
CC associated with peripheral diseases including blood loss of any kind,
CC renal failure, conditions associated with anaemia, and neurological and
CC neuropsychiatric manifestations including haematological and
CC non-haematological malignancies/cancer, symptoms or complications in
CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This

CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTFSCHFGPLTWCKPQGG 20
RESULT 26
ID AAU74486 standard; Peptide; 20 AA.
XX AAU74486;
XX
DT 09-APR-2002 (first entry)
XX
DE Human erythropoietin neuroprotective peptide EMP-34.
XX
KW Neuroprotective peptide; human; erythropoietin; neurotoxicity; anaemia;
KW erythropoietin receptor; EPO receptor; neurodegeneration; prion disease;
KW neurological damage; neurodegenerative disorder; neurological disorder;
KW psychiatric disorder; blood loss; renal failure; cancer; HIV;
KW human immunodeficiency virus; haematology; autoimmune disease;
KW inflammatory disorder; infectious disease; EMP-34.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="Acetyl-Glycine"
FV
XX W0200:9178C-AI.
XX
XX 06-DEC-2001.
XX
XX 23-MAY-2001; 2001WO-US16654.
XX
XX 26-MAY-2000; 2000US-207654P.
XX
XX (ORTH : ORTHO MCNEIL PHARM INC.
XX
XX Smith-Swintosky V, Renzi M, Piata-Salaman C, Colliffe L, Farrell F;
XX Johnson DL;
XX
XX WPI; 2002-114307/15.
XX
XX Treating patients having condition mediated by neurotoxicity,
XX neurodegeneration or neurological damage, involves administering to
XX patient a peptide comprising monomeric peptides that bind to
XX erythropoietin receptor -
XX
XX Claim 14; Page 41; 75pp; English.
XX
XX The invention relates to a method for treating a patient with a condition
XX mediated by neurotoxicity, neurodegeneration or neurological damage,
XX involving administering a peptide comprising one or more monomeric
XX peptides that bind to the human erythropoietin (EPO) receptor. The method
XX is useful for treating acute and chronic neurodegenerative disorders
XX including cerebral ischaemia or infarction, Alzheimer's disease, Pick's
XX disease, diffuse Lewy body disease, Shy-Drager syndrome, amyotrophic
XX lateral sclerosis, Huntington's disease, Parkinson's disease, Gilles De
XX La Tourette's disease, Tay-Sachs disease, and prion diseases including
XX Creutzfeldt-Jakob and Kuru, neurological and psychiatric manifestations
XX associated with peripheral diseases including blood loss of any kind,
XX renal failure, conditions associated with anaemia, and neurological and
XX neuropsychiatric manifestations including haematological and
XX non-haematological malignancies/cancer, symptoms or complications in

CC patients receiving chemotherapy, inflammatory and infectious disorders
CC such as human immunodeficiency viral infections, and chronic systemic
CC autoimmune diseases such as systemic lupus erythematosus. The method is
CC also useful for prevention of plexopathies and neuropathies. This
CC sequence represents a human erythropoietin neuroprotective peptide of the
CC invention.
XX
SQ Sequence 20 AA;
Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTFSCHFGPLTWCKPQGG 20
RESULT 27
ID ABB72814 standard; Peptide; 20 AA.
XX ABB72814;
XX
DT 05-APR-2002 (first entry)
XX
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:87.
XX
KW Modified peptide; mimetic; FC domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritis; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX W0200183525-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US14310.
XX
XX 03-MAY-2000; 2000US-0563286.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
XX diabetic retinopathy, obesity, sleep disorders and infertility -
XX
XX Claim 39; Page 41; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
XX multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
XX cytostatic, antirheumatic, antiarthritis, antidiabetic, ophthalmological,
XX antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
XX neuroprotective activities. (I) can be used as a therapeutic or
XX prophylactic agent as well as for screening purposes. (I) is useful for
XX diagnosing diseases characterised by dysfunction of their associated
XX protein of interest, for identifying normal or abnormal proteins of
XX interest, as a part of diagnostic kit to detect the presence of their

CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 20 AA;
 SQ

Query Match 95.1%; Score 117; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 28
 ABB72840
 ID ABB72840 standard; Peptide: 20 AA.
 XX
 AC ABB72840;
 XX
 DT 05-APR-2002 (first entry)
 XX
 DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:1025.
 XX
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytotstatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaeamic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001WO-US14310.
 XX
 PR 03-MAY-2000; 2000US-0563286.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX
 DR WPI; 2002-130313/17.
 XX
 PT Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX
 PS Claim 39; Page 42; 176pp; English.
 CC
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,

CC cytotstatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaeamic, anorectic, antiinfertility, haemostatic, dermatological, and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 20 AA;
 SQ

Query Match 95.1%; Score 117; DB 23; Length 20;
 Best Local Similarity 95.0%; Pred. No. 3.1e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 29
 ABB57650
 ID ABB57650 standard; Peptide: 20 AA.
 XX
 AC ABB57650;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE Erythropoietin receptor peptide agonist.
 XX
 KW Antirheumatic; antiarthritic; osteopathic; cartilage disorder;
 KW insulin-like growth factor; IGF; binding protein; IGFBP;
 KW rheumatoid arthritis; osteoarthritis; erythropoietin; agonist.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 6..15
 XX
 PN WO200187323-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US15904.
 XX
 PR 16-MAY-2000; 2000US-204490P.
 PR 15-NOV-2000; 2000US-248985P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dubaque Y, Filvaroff EH, Lowman HB;
 XX
 DR WPI; 2002-082942/11.
 XX
 PT Treating cartilage disorders including cartilage damage by injury or
 PT degenerative cartilaginous disorders, by contacting cartilage with
 PT insulin-like growth factor analog with altered affinity for IGF-binding
 PT proteins -
 XX
 PS Example 1; Page 40; 136pp; English.
 XX

CC The present invention relates to a method for treating cartilage disorders. The method comprises contacting cartilage with an active agent such as insulin-like growth factor (IGF-1) analog with a binding affinity preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1 analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a IGFBP displacer peptide that prevents the interaction of IGF with an IGFBP and does not bind to human IGF receptor. The method is useful for treating cartilage disorders (CD), including degenerative CD, articular CD such as rheumatoid arthritis and osteoarthritis. The present sequence CC was used to illustrate the invention.

XX Sequence 20 AA;

SQ Query Match 95.1%; Score 117; DB 23; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
AAV13638
ID AAY13638 standard; peptide; 22 AA.
XX AC AAY13638;
XX DT 06-SEP-1999 (first entry)
XX DE Erythropoietin receptor (EPO-R) binding peptide.
XX KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS; dialysis; anaemia; autoimmune disease; chronic inflammatory disease; malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss; spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX OS Synthetic.
XX PN WC9643749-A1.
XX PD 19-DEC-1996.
XX PF 07-JUN-1996; 96WO-US09810.
XX PR 07-JUN-1995; 95US-0484635.
XX PR 07-JUN-1995; 95US-0484631.
XX PR 19-NOV-1993; 93US-0155940.
XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
XX PA (CORJ) JOHNSON & JOHNSON CORP.
XX PA (ORTH) ORTHO PHARM CORP.
XX PI Chang RS, Dower WJ, Johnson D, Jolliffe LX, Kashyap AK;
XX PI Mulcahy L, Wrighton NC;
XX DR WPI; 1997-052225/05.
XX Erythropoietin receptor binding peptide - useful for treating disorders characterised by deficiency of EPO, or low or defective red blood cell population
XX Claim 6; Page 68; 95pp; English.
XX The invention describes a peptide of 10-40 amino acid residues which binds to erythropoietin (EPO) receptor and which includes the amino acid sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg, His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally, the peptide may be cyclised or dimerised. The peptide can be used to treat a patient having a disorder characterised by a deficiency of EPO or a low or defective red blood cell population. It can be used to treat end stage renal failure or dialysis; anaemia associated with AIDS,

CC autoimmune disease, chronic inflammatory diseases or malignancy; beta-thalassemia; cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute blood loss; aging; and neoplastic disease states accompanied by abnormal erythropoiesis. The peptides can also be used as reagents for detecting EPO receptors on living cells, in biological fluids, in tissue homogenates, etc. Sequences AAV13624-661 represent CC specific examples of EPO-R binding peptides.

XX Sequence 22 AA;

SQ Query Match 95.1%; Score 117; DB 18; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 3 GGTYSCHFGPLTWCKPQGG 22

RESULT 31
AAB17041
ID AAB17041 standard; Peptide; 22 AA.
XX AC AAB17041;
XX DT 31-OCT-2000 (first entry)
XX DE EPO-mimetic peptide sequence SEQ ID NO:97.
XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF; immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.
XX OS Synthetic.
XX PN WO200024782-A2.
XX PD 04-MAY-2000.
XX PF 25-OCT-1999; 99WO-US25044.
XX PR 23-OCT-1998; 99US-0105371.
XX PR 22-OCT-1999; 99US-0428082.
XX PA (AMGE-) AMGEN INC.
XX PI Feige U, Liu C, Cheetham J, Boone TC;
XX DR WPI; 2000-350702/30.
XX Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and autoimmune diseases -
XX Claim 13; Page 229; 608pp; English.
XX The present invention describes composition of matter (I) comprising an Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 CC where P1, P2, P3, and P4 = are each independently sequences of CC pharmacologically active peptides; L1, L2, L3, and L4 = are each CC independently linkers; and a, b, c, d, e, and f = are each independently 0 or 1, provided that at least 1 of a and b is 1. The composition can CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive CC activities. DNAs, vectors and host cells from the present invention can CC be used for producing pharmaceutical compositions. The compositions are CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.

XX Sequence 22 AA;

Query Match 95.1%; Score 117; DB 21; Length 22;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 32
 ABB72824
 ID ABB72824 standard; Peptide; 22 AA.

XX ABB72824;

XX 05-APR-2002 (first entry)

DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:97.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMR;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14310.

XX 03-MAY-2000; 2000US-0563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX Claim 39; Page 41; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful

CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 22 AA;

Query Match 95.1%; Score 117; DB 23; Length 22;
 Best Local Similarity 95.0%; Pred. No. 3.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| ||||| |||||
 Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 33

AA26551

ID AA26551 standard; peptide; 23 AA.

XX AA26551;

XX 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.

XX Synthetic.

XX WO9640749-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09810.

XX 07-JUN-1995; 95US-0484635.

XX 07-JUN-1995; 95US-0484631.

XX 19-NOV-1993; 93US-0155940.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX (JOHJ) JOHNSON & JOHNSON CORP.

XX (ORTH) ORTHO PHARM CORP.

XX Chang RS, Dower WJ, Johnson D, Jolliffe LK, Kashyap AK;

XX Mulcahy L, Wrighton NC;

XX WPI; 1997-052225/05.

XX Erythropoietin receptor binding peptide - useful for treating

PT disorders characterised by deficiency of EPO, or low or defective

PT red blood cell population

XX Disclosure; Page 28; 95pp; English.

XX The invention describes a peptide of 10-40 amino acid residues which

CC binds to erythropoietin (EPO) receptor and which includes the amino acid

CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,

CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically

CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,

CC the peptide may be cyclised or dimerised. The peptide can be used to

CC treat a patient having a disorder characterised by a deficiency of EPO

CC or a low or defective red blood cell population. It can be used to treat
 CC end stage renal failure or dialysis; anemia associated with AIDS,
 CC autoimmune disease, chronic inflammatory diseases or malignancy;
 CC beta-thalassemia; cystic fibrosis; early anaemia of prematurity; spinal
 CC cord injury; acute blood loss; aging; and neoplastic disease states
 CC accompanied by abnormal erythropoiesis. The peptides can also be used as
 CC reagents for detecting EPO receptors on living cells, in biological
 CC fluids, in tissue homogenates, etc. Sequences AAR26352-548 are
 CC representative peptides falling within the above peptide motif and
 CC isolated during the affinity selection process.

XX
 SQ Sequence 23 AA;

Query Match 95.1%; Score 117; DB 18; Length 23;

Best Local Similarity 95.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 34

AAB17038
 ID AAB17038 standard; Peptide; 23 AA.

AC AAB17038;

DT 31-OCT-2000 (first entry)

DE EPO-mimetic peptide sequence SEQ ID NO:94.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

OS Synthetic.

PN WO200024782-A2.

PD 04-MAY-2000.

PF 25-OCT-1999; 99WO-US25044.

PR 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

PA (AMGE-) AMGEN INC.

PI Feige U, Liu C, Cheetham J, Boone TC;

DR WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -

PS Claim 13; Page 227; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are

CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69536 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.

XX Sequence 23 AA;

Query Match 95.1%; Score 117; DB 21; Length 23;

Best Local Similarity 95.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 35

AAB17042

ID AAB17042 standard; Peptide; 23 AA.

AC AAB17042;

DT 31-OCT-2000 (first entry)

DE EPO-mimetic peptide sequence SEQ ID NO:98.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

OS Synthetic.

PN WO200024782-A2.

PD 04-MAY-2000.

PF 25-OCT-1999; 99WO-US25044.

PR 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

PA (AMGE-) AMGEN INC.

PI Feige U, Liu C, Cheetham J, Boone TC;

DR WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -

PS Claim 13; Page 229; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are

CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.

XX Sequence 23 AA;

SQ Query Match 95.1%; Score 117; DB 21; Length 23;

Best Local Similarity 95.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTASCHFGPLTWCKPQGG 20

DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 36

ABB72821
 ID ABB72821 standard; Peptide; 23 AA.

AC ABB72821;

DT 05-APR-2002 (first entry)

DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:94.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

X: WO200183525-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14310.

XX PR 03-MAY-2000; 2000US-0563286.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX DR WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX Claim 39; Page 41; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their

CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 23 AA;

Query Match 95.1%; Score 117; DB 23; Length 23;

Best Local Similarity 95.0%; Pred. No. 3.5e-09;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGTASCHFGPLTWCKPQGG 20

DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 37

ABB72825
 ID ABB72825 standard; Peptide; 24 AA.

XX AC ABB72825;

DT 05-APR-2002 (first entry)

DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:98.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX PN WO200183525-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US14310.

XX PR 03-MAY-2000; 2000US-0563286.

XX PA (AMGE-) AMGEN INC.

XX PI Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX DR WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX Claim 39; Page 41; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,

CC cytostatic, antirheumatic, antiarthritic, antidiabetic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The EPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

SQ Sequence 24 AA;

Query Match 95.1%; Score 117; DB 23; Length 24;
 Best Local Similarity 95.0%; Pred. No. 3.7e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 38
 ABB73394
 ID ABB73394 standard; Peptide; 25 AA.

XX ABB73394;

DT 05-APR-2002 (first entry)

DE EPO-mimetic peptide SEQ ID NO:1034.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPC; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNF;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

PN WO200183525-A2.

XX 08-NOV-2001.

PJ 02-MAY-2001; 2001WO-US14310.

PF 03-MAY-2000; 2000US-0563286.

PR (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

PI WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating

PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -
 XX Disclosure; Page 90; 176pp; English.
 PS
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The EPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 25 AA;

Query Match 95.1%; Score 117; DB 23; Length 25;
 Best Local Similarity 95.0%; Pred. No. 3.8e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
 ||| ||||| ||||| |||||
 DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 39

AAAB17930

ID AAB17930 standard; Peptide; 26 AA.

XX AAB17930;

DT 31-OCT-2000 (first entry)

DE EPO-mimetic peptide sequence SEQ ID NO:1034.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

OS Synthetic.

PN WO200024782-A2.

XX 04-MAY-2000.

PF 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

PR 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
XX
PS Disclosure; Page 559; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 26 AA;
Query Match 95.1%; Score 117; DB 21; Length 26;
Best Local Similarity 95.0%; Pred. No. 4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 1 GGTYSCHFGPLTWCKPQGG 20
||| |||||
RESULT 40
AAB17313
ID AAB17313 standard; Peptide: 36 AA.
XX
AC AAB17313;
XX
DT 31-OCT-2000 (first entry)
XX
DE EMP-Fc fusion construction peptide SEQ ID NO:403.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
PR 22-OCT-1999; 99US-0428082.
XX
XX (AMGE-) AMGEN INC.
PA
PI Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX

PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
XX
PS Example 3; Page 337; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 36 AA;
Query Match 95.1%; Score 117; DB 21; Length 36;
Best Local Similarity 95.0%; Pred. No. 5.4e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
||| |||||
Db 12 GGTYSCHFGPLTWCKPQGG 31
||| |||||
RESULT 41
AAB73407
ID ABB73407 standard; Peptide: 36 AA.
XX
AC ABB73407;
XX
DT 05-APR-2002 (first entry)
XX
DE EPO mimetic peptide gene construction related peptide SEQ ID NO:403.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianemic; anorectic; antinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
XX (AMGE-) AMGEN INC.
PA
PI Feige U, Liu C, Cheetham JC, Boone TC, Gudus JM;
XX

XX WPI: 2002-130313/17.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility .
 XX Example 3; Page 114; 176pp; English.
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.
 XX Sequence 36 AA;
 SQ
 Query Match 95.1%; Score 117; DB 23; Length 36;
 Best Local Similarity 95.0%; Pred. No. 5.4e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 12 GGTYSCHFGPLTWCKPQGG 31
 RESULT 42
 AAB17312
 ID AAB17312 standard; Peptide; 39 AA.
 AC AAB17312;
 XX 31-OCT-2000 (first entry)
 DE FC-EMP fusion construction peptide SEQ ID NO:395.
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW TNF-alpha inhibitor; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200024782-A2.
 XX 04-MAY-2000.
 XX 25-OCT-1999; 99WO-US25044.
 XX 23-OCT-1998; 98US-0105371.
 XX 22-OCT-1999; 99US-0428082.

(AMGE-) AMGEN INC.
 Feige U, Liu C, Cheetham J, Boone TC;
 WPI: 2000-350702/30.
 Novel composition of matter comprising an Fc domain and
 pharmacologically active peptides, useful for treating cancer and
 autoimmune diseases .
 Example 3; Page 335; 608pp; English.
 The present invention describes composition of matter (I) comprising an
 Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAB69443
 CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.
 XX Sequence 39 AA;
 SQ
 Query Match 95.1%; Score 117; DB 21; Length 39;
 Best Local Similarity 95.0%; Pred. No. 5.8e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGTASCHFGPLTWCKPQGG 20
 DB 8 GGTYSCHFGPLTWCKPQGG 27
 RESULT 43
 ABB73406
 ID ABB73406 standard; Peptide; 39 AA.
 AC ABB73406;
 XX 05-APR-2002 (first entry)
 DE EPO mimetic peptide gene construction related peptide SEQ ID NO:395.
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200183525-A2.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14310.

XX 03-MAY-2000; 2000US-0563286.
 PR (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility -

PS Example 3; Page 112; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianæmic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising
 CC EPO-mimetic compounds are useful for treating disorders characterised by
 CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention.

XX Sequence 39 AA;

Query Match 95.1%; Score 117; DB 23; Length 39;

Best Local Similarity 95.0%; Pred. No. 5.8e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

DB 8 GGTYSCHFGPLTWCKPQGG 27

RESULT 44

ABB17036

ID AAB17036 standard; Peptide; 40 AA.

XX AAB17036;

DT 31-OCT-2000 (first entry)

DE EPO-mimetic peptide sequence SEQ ID NO:92.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.

XX Synthetic.

XX WO200024782-A2.

XX 04-MAY-2000.

XX

PF 25-OCT-1999; 99WO-US25044.

XX 23-OCT-1998; 98US-0105371.

XX 22-OCT-1999; 99US-0428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -

XX Claim 13; Page 226; 608pp; English.

XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiaesthetic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.

XX The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAB69443
 CC to AAB69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.

XX Sequence 40 AA;

Query Match 95.1%; Score 117; DB 21; Length 40;

Best Local Similarity 95.0%; Pred. No. 5.9e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20

DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 45

ABB72819

ID ABB72819 standard; Peptide; 40 AA.

XX ABB72819;

XX 05-APR-2002 (first entry)

DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:92.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
 KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianæmic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory diseases; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.

XX Homo sapiens.

OS Synthetic.

XX

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PN WO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14310.
XX
PR 03-MAY-2000; 2000US-0563286.
XX
PA (AMGE-) AMGEN INC.
XX
P1 Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX
DR WPI; 2002-130313/17.
XX
PT Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility -
XX
PS Claim 39; Page 41; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumor, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The EPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 40 AA;
Query Match 95.1%; Score 117; DB 23; Length 40;
Best Local Similarity 95.0%; Pred. No. 5.9e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
DQ 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 46
AAE17037
ID AAB17037 standard; Peptide; 41 AA.
XX
AC AAB17037;
XX
DT 31-OCT-2000 (first entry)
XX
DE EPO-mimetic peptide sequence SEQ ID NO:93.
XX
KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
KW autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
KW immunosuppressive; EPO; iPO; C11A4; mimetic; IL-1; TNF; antagonist;
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
KW vascular endothelial growth factor; matrix metalloproteinase;
KW asthma; thrombosis; pharmaceutical.
XX
OS Synthetic.
XX
PN WO200024782-A2.
XX
PD 04-MAY-2000.
XX
PF 25-OCT-1999; 99WO-US25044.
XX
PR 23-OCT-1998; 98US-0105371.
XX
PR 22-OCT-1999; 99US-0428082.
XX
PA (AMGE-) AMGEN INC.
XX
P1 Feige U, Liu C, Cheetham J, Boone TC;
XX
DR WPI; 2000-350702/30.
XX
PT Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases -
XX
PS Claim 13; Page 227; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiaesthetic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 41 AA;
Query Match 95.1%; Score 117; DB 21; Length 41;
Best Local Similarity 95.0%; Pred. No. 6.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGTASCHFGPLTWCKPQGG 20
DQ 1 GGTYSCHFGPLTWCKPQGG 20
RESULT 47
ABB72820
ID ABB72820 standard; Peptide; 41 AA.
XX
AC ABB72820;
XX
DT 05-APR-2002 (first entry)
XX
DE Erythropoietin (EPO) mimetic peptide SEQ ID NO:93.
XX
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumor; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
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PR 23-OCT-1998; 98US-0105371.
FR 22-OCT-1999; 99US-0428082.
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham J, Boone TC;
XX WPI; 2000-350702/30.
XX
XX Novel composition of matter comprising an Fc domain and
PT pharmacologically active peptides, useful for treating cancer and
PT autoimmune diseases.
XX
XX Claim 13; Page 228; 608pp; English.
XX
CC The present invention describes composition of matter (I) comprising an
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
CC where P1, P2, P3, and P4 = are each independently sequences of
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
CC independently linkers; and a, b, c, d, e, and f = are each independently
CC c or i, provided that at least 1 of a and b is 1. The composition can
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
CC activities. DNAs, vectors and host cells from the present invention can
CC be used for producing pharmaceutical compositions. The compositions are
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
CC The use of an Fc domain (rather than a Fab domain) can provide a longer
CC half-life or incorporate functions such as Fc receptor binding, protein
CC A binding, complement fixation, and possibly placental transfer. AAA69443
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
CC sequences used in the exemplification of the present invention.
XX
XX Sequence 46 AA;
SQ
Query Match 95.1%; Score 117; DB 21; Length 46;
Best Local Similarity 95.0%; Pred. No. 6.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 50
AAB72822
ID ABB72822 standard; Peptide: 46 AA.
XX
AC ABB72822;
XX
DT 05-APR-2002 (first entry)
XX
XX Erythropoietin (EPO) mimetic peptide SEQ ID NO:95.
XX
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
KW antianaemic; anorectic; antinfertility; haemostatic; dermatological;
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KW sleep disorder; neurological degenerative disease; anaemia;
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KW Fanconi's syndrome.
XX
XX Homo sapiens.
OS
CS Synthetic.
XX
XX PN WO200183525-A2.
XX

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PD 08-NOV-2001.
PF 02-MAY-2001; 2001WO-US14310.
XX
XX 03-MAY-2000; 2000US-0563286.
XX
XX (AMGE-) AMGEN INC.
XX
XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;
XX WPI; 2002-130313/17.
XX
XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Claim 39; Page 41; 176pp; English.
XX
CC The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising,
CC EPO-mimetic compounds are useful for treating disorders characterised by
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention.
XX
XX Sequence 46 AA;
SQ
Query Match 95.1%; Score 117; DB 23; Length 46;
Best Local Similarity 95.0%; Pred. No. 6.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

Search completed: November 5, 2003, 19:05:31
Job time : 42 secs

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ALIGNMENTS

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RESULT 1
US-08-484-635-52
; Sequence 52, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-52

Query Match 100.0%; Score 123; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 2
US-08-484-631-52
; Sequence 52, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-52

Query Match 100.0%; Score 123; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
```

```
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-52

Query Match 100.0%; Score 123; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 3
US-08-827-570-52
; Sequence 52, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-52

Query Match 100.0%; Score 123; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 4
US-08-484-635-189
; Sequence 189, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-189

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 5
US-08-484-635-247
; Sequence 247, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
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NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-484-635-247

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTASCHFGPLTWCKPQGG 20

RESULT 6
US-08-484-635-248
; Sequence 248, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"

US-08-484-635-248
Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTASCHFGPLTWCKPQGG 20

RESULT 6
US-08-484-635-248
; Sequence 248, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"

US-08-484-635-248
Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTASCHFGPLTWCKPQGG 20

RESULT 7
US-08-484-635-249
; Sequence 249, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"

US-08-484-635-249
Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTASCHFGPLTWCKPQGG 20

RESULT 8
US-08-484-635-250
; Sequence 250, Application US/08484635

Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"
US-08-484-635-250

Query Match 96.7%; Score 119; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 9

US-08-484-631-189
Sequence 189, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda

TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-189

Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 10

US-08-484-631-247
Sequence 247, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-484-631-247
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Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
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RESULT 11
US-08-484-631-248
; Sequence 248, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Colliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-484-631-248
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Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTASCHFGPLTWCKPQGG 20
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RESULT 12
US-08-484-631-249
; Sequence 249, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Colliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"
US-08-484-631-249

Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 13
US-08-484-631-250
; Sequence 250, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"

US-08-484-631-250

Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 14
US-08-827-570-189
; Sequence 189, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-189

Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTTSCHFGPLTWCKPQGG 20

RESULT 15

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US-08-827-570-247
; Sequence 247, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street, Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-nitro-phenylalanine"
US-08-827-570-247
Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 16
US-08-827-570-248
; Sequence 248, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
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; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = para-amino-phenylalanine"
US-08-827-570-248
Query Match 96.7%; Score 119; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 8.4e-11;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 17
US-08-827-570-249
; Sequence 249, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
```


1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Townsend and Townsend and Crew
3 STREET: One Market Plaza, Steuart Street Tower
4 CITY: San Francisco
5 STATE: California
6 COUNTRY: USA
7 ZIP: 94105-1492
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: Patent In Release #1.0, Version #1.30
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/827,570
16 FILING DATE:
17
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/484,635
21 FILING DATE: 07-JUN-1995
22 APPLICATION NUMBER: US 08/155,940
23 FILING DATE: 19-NOV-1993
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Garrett-Wackowski, Eugenia
26 REGISTRATION NUMBER: 37,330
27 REFERENCE/DOCKET NUMBER: 16528A-43-1-1
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (415) 543-9600
30 TELEFAX: (415) 543-5043
31 INFORMATION FOR SEQ ID NO: 249:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 20 amino acids
34 TYPE: amino acid
35 STRANDEDNESS:
36 TOPOLOGY: linear
37 MOLECULE TYPE: peptide
38 FEATURE:
39 NAME/KEY: Modified-site
40 LOCATION: 4
41 OTHER INFORMATION: /product= "OTHER"
42 OTHER INFORMATION: /note= "Xaa = para-fluoro-phenylalanine"
43
44 US-08-827-570-249
45
46 Query Match 96.7%; Score 119; DB 2; Length 20;
47 Best Local Similarity 95.0%; Pred. No. 8.4e-11;
48 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
49
50 Qy 1 GGTASCHFGPLTWCKPQQG 20
51 ||| |||||
52 Db 1 GGTXSCHFGPLTWCKPQQG 20
53
54 RESULT 18
55 US-08-827-570-250
56 Sequence 250, Application US/08827570
57 Patent No. 5986047
58 GENERAL INFORMATION:
59 APPLICANT: Wrighton, Nicholas C.
60 APPLICANT: Dower, William J.
61 APPLICANT: Chang, Ray S.
62 APPLICANT: Kashyap, Arun K.
63 APPLICANT: Jolliffe, Linda K.
64 APPLICANT: Johnson, Dana
65 APPLICANT: Mulcahy, Linda
66 TITLE OF INVENTION: Compounds and Peptides That Bind to the
67 NUMBER OF SEQUENCES: 259
68 CORRESPONDENCE ADDRESS:
69 ADDRESSEE: Townsend and Townsend and Crew
70 STREET: One Market Plaza, Steuart Street Tower
71 CITY: San Francisco
72 STATE: California
73 COUNTRY: USA
74 ZIP: 94105-1492

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Version #1.30
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/827,570
8 FILING DATE:
9
10 CLASSIFICATION:
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/484,635
13 FILING DATE: 07-JUN-1995
14 APPLICATION NUMBER: US 08/155,940
15 FILING DATE: 19-NOV-1993
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Garrett-Wackowski, Eugenia
18 REGISTRATION NUMBER: 37,330
19 REFERENCE/DOCKET NUMBER: 16528A-43-1-1
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (415) 543-9600
22 TELEFAX: (415) 543-5043
23 INFORMATION FOR SEQ ID NO: 250:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 20 amino acids
26 TYPE: amino acid
27 STRANDEDNESS:
28 TOPOLOGY: linear
29 MOLECULE TYPE: peptide
30 FEATURE:
31 NAME/KEY: Modified-site
32 LOCATION: 4
33 OTHER INFORMATION: /product= "OTHER"
34 OTHER INFORMATION: /note= "Xaa = 3,5-dibromo-tyrosine"
35
36 US-08-827-570-250
37
38 Query Match 96.7%; Score 119; DB 2; Length 20;
39 Best Local Similarity 95.0%; Pred. No. 8.4e-11;
40 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
41
42 Qy 1 GGTASCHFGPLTWCKPQQG 20
43 ||| |||||
44 Db 1 GGTXSCHFGPLTWCKPQQG 20
45
46 RESULT 19
47 US-08-484-135-8
48 Sequence 8, Application US/08484135
49 Patent No. 5767078
50 GENERAL INFORMATION:
51 APPLICANT: Johnson, Dana L.
52 APPLICANT: Zivin, Robert A.
53 TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
54 NUMBER OF SEQUENCES: 93
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: Frank S. DiGiglio
57 STREET: 400 Garden City Plaza
58 CITY: Garden City
59 STATE: New York
60 COUNTRY: U.S.A..
61 ZIP: 11530
62
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible
66 OPERATING SYSTEM: PC-DOS/MS-DOS
67 SOFTWARE: Patent In Release #1.0, Version #1.25
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/08/484,135
70 FILING DATE: 07-JUN-1995
71 CLASSIFICATION: 514
72 ATTORNEY/AGENT INFORMATION:
73 NAME: DiGiglio, Frank S.
74 REGISTRATION NUMBER: 31,346
75 REFERENCE/DOCKET NUMBER: 9594

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-8

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 20

US-08-484-135-20
; Sequence 20, Application US/08-84135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-20

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 21

US-08-484-135-42

; Sequence 42, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Frank S. DiGiglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-135-42

Query Match 95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 22

US-08-484-635-8
; Sequence 8, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-8

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20

RESULT 23
US-08-484-635-190
; Sequence 190, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-8

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
Db      1 GGTYSCHFGPLTWCKPQGG 20
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```
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-190

Query Match          95.1%; Score 117; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWCKPQGG 20
      ||| ||||| ||||| |||||
Db      1 GGTFSCHFGPLTWCKPQGG 20

RESULT 24
US-08-484-631-8
; Sequence 8, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-8

Query Match          95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-8

Query Match 95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 28
US-08-827-570-190
; Sequence 190, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcany, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940

FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-190

Query Match 95.1%; Score 117; DB 2; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||||||||||
Db 1 GGTFSCHFGPLTWCKPQGG 20

RESULT 29
US-08-905-310-2
; Sequence 2, Application US/08905310
; Patent No. 6077939
; GENERAL INFORMATION:
; APPLICANT: Wei, Ziping
; APPLICANT: Menon-Rudolph, Sunitha
; APPLICANT: Ghosh-Dastidar, Pradip
; TITLE OF INVENTION: Polypeptides Having a Single Covalently Bound
; TITLE OF INVENTION: N-Terminal Water-Soluble Polymer, and Related Methods,
; TITLE OF INVENTION: Compositions and Kits
; FILE REFERENCE: SEQUENCE LISTING OPT 843
; CURRENT APPLICATION NUMBER: US/08/905,310
; CURRENT FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide fragment
US-08-905-310-2

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||||||||||
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 30
US-08-825-852-34
; Sequence 34, Application US/08825852
; Patent No. 6121416
; GENERAL INFORMATION:
; APPLICANT: Clark, Ross G1
; APPLICANT: Lowman, Henry B.
; APPLICANT: Robinson, Iain C.A.F.
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,852
FILING DATE: 04-Apr-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-825-852-34

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 31
US-08-786-690-1
Sequence 1, Application US/08786690
Patent No. 6221608
GENERAL INFORMATION:
APPLICANT: Middleton, Steven
APPLICANT: Johnson, Dana
APPLICANT: McMahon, Frank
APPLICANT: Mulkahy, Linda
APPLICANT: Jolliffe, Linda
TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
TITLE OF INVENTION: ERYTHROPOIETIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,690
FILING DATE: 08 August 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-821
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-2806
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
US-08-786-690-1

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 32
US-08-786-690-4
Sequence 4, Application US/08786690
Patent No. 6221608
GENERAL INFORMATION:
APPLICANT: Middleton, Steven
APPLICANT: Johnson, Dana
APPLICANT: McMahon, Frank
APPLICANT: Mulkahy, Linda
APPLICANT: Jolliffe, Linda
TITLE OF INVENTION: METHOD FOR PURIFICATION AND USE OF
TITLE OF INVENTION: ERYTHROPOIETIN BINDING PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,690
FILING DATE: 08 August 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-821
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-524-2806
TELEFAX: 732-524-2808
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ANTI-SENSE: NO
US-08-786-690-4

Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 33

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US-09-052-888-34
; Sequence 34, Application US/09052888
; Patent No. 6251865
; GENERAL INFORMATION:
; APPLICANT: Clark, Ross G1
; APPLICANT: Lowman, Henry B.
; APPLICANT: Robinson, Iain C.A.F.
; TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
; NUMBER OF SEQUENCES: 109
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 31-Mar-1998
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hawak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1071P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-052-888-34
Query Match 95.1%; Score 117; DB 3; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.6e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DI 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 34
US-08-484-635-20
; Sequence 20, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-484-635-20
Query Match 95.1%; Score 117; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 35
US-08-484-631-20
; Sequence 20, Application US/08484631
; Patent No. 5810851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US 08-484-631-20

Query Match 95.1%; Score 117; DB 2; Length 23;
Best Local Similarity 95.0%; Pred. No. 1.9e-13;
Matches 19; Conservative 0; Mismatches 1; Indels 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 36
US-08-827-570-20
; Sequence 20, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-5043
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-20

Query Match 95.1%; Score 117; DB 2; Length 23;

Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 37
US-08-484-635-192
; Sequence 192, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-192

Query Match 91.1%; Score 112; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 38
US-08-484-635-194
; Sequence 194, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.


```

; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-635-194

Query Match 91.1%; Score 112; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFQPLTWCKPQGG 20

RESULT 39
US-08-484-631-192
; Sequence 192, Application US/08484631
; Patent No. 5810851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California

```

```

; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-192

Query Match 91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGTYSCHFQPLTWCKPQGG 20

RESULT 40
US-08-484-631-194
; Sequence 194, Application US/08484631
; Patent No. 5810851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993

```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-631-194

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
      ||| ||||| ||||| |||
Db      : GGTYSCHFGLATWVCKPQGG 20

RESULT 41:
US-08-827-570-192
; Sequence 192, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-192

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
      ||| ||||| ||||| |||
Db      1 GGTYSCHFGLATWVCKPQGG 20

RESULT 42:
US-08-827-570-194
; Sequence 194, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-827-570-194

Query Match          91.1%; Score 112; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGTASCHFGPLTWVCKPQGG 20
      ||| ||||| ||||| |||
Db      1 GGTYSCHFGLATWVCKPQGG 20
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RESULT 43
US-08-484-635-18
; Sequence 18, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-484-635-18

Query Match 90.2%; Score 111; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 2 GTYSCHFGLTWCKPQGG 20

RESULT 44
US-08-484-635-193
; Sequence 193, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

```

```

; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-484-635-193

Query Match 90.2%; Score 111; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTYSCHFAPLTWCKPQGG 20

RESULT 45
US-08-484-631-18
; Sequence 18, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-484-631-18

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 GTYSCHFGPLTWCKPQGG 20

RESULT 46
US-08-484-631-193
Sequence 193, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 193:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-193

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GGTYSCHFGPLTWCKPQGG 20

RESULT 47
US-08-827-570-18
Sequence 18, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = N-acetyl-glycine"
US-08-827-570-18

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 94.7%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2 GTYSCHFGLTWVCKPQGG 20

RESULT 48
US-08-827-570-193
; Sequence 193, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,310
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-193

Query Match 90.2%; Score 111; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.2e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWVCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFAPLTWVCKPQGG 20

RESULT 49
US-08-484-635-191
; Sequence 191, Application US/08484635
; Patent No. 5773569
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/484,635
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION NUMBER: 37,310
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-635-191

Query Match 88.6%; Score 109; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GGTYSCHFAPLTWVCKPQGG 20

RESULT 50
US-08-484-631-191
; Sequence 191, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:

Query Match 88.6%; Score 109; DB 2; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.3e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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D5 1 GGTYSCHFGALTWCKPQGG 20

Search completed: November 5, 2003, 19:07:53
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:06:49 ; Search time 29 Seconds
(without alignments)
118.448 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGPLTWCKPGG 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	119	96.7	20	12	US-09-863-600E-41
8	119	96.7	20	12	US-09-863-600E-42
9	117	95.1	20	11	US-09-858-935B-66
10	117	95.1	20	12	US-09-863-600E-8
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47	51	41.5	23	11	US-09-858-935B-46	Sequence 46, Appl
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49	49	39.8	24	9	US-09-864-761-40377	Sequence 40377, A
50	48	39.0	42	9	US-09-864-761-48118	Sequence 48118, A
51	47	38.2	11	11	US-09-858-935B-108	Sequence 108, Appl
52	46.5	37.8	73	11	US-09-910-082A-301	Sequence 301, Appl
53	46	37.4	12	12	US-10-271-343-15	Sequence 15, Appl
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55	46	37.4	19	11	US-09-858-935B-27	Sequence 27, Appl
56	46	37.4	19	11	US-09-858-935B-33	Sequence 33, Appl
57	46	37.4	293	12	US-10-145-206-123	Sequence 123, Appl
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74	45	36.6	18	11	US-09-858-935B-39	Sequence 39, Appl
75	45	36.6	21	11	US-09-858-935B-40	Sequence 40, Appl
76	45	36.6	21	11	US-09-858-935B-42	Sequence 42, Appl
77	45	36.6	28	11	US-09-932-613-165	Sequence 165, Appl
78	45	36.6	28	12	US-09-932-322-165	Sequence 165, Appl
79	45	36.6	290	9	US-09-764-853-513	Sequence 513, Appl
80	45	36.6	702	15	US-10-156-761-9689	Sequence 9689, Appl
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82	44.5	36.2	337	12	US-10-321-807-6	Sequence 6, Appl
83	44.5	36.2	337	15	US-10-225-567A-591	Sequence 591, Appl
84	44	35.8	14	11	US-09-858-935B-29	Sequence 29, Appl
85	44	35.8	14	11	US-09-858-935B-30	Sequence 30, Appl
86	44	35.8	14	11	US-09-858-935B-48	Sequence 48, Appl
87	44	35.8	14	11	US-09-858-935B-50	Sequence 50, Appl
88	44	35.8	58	15	US-10-106-698-5090	Sequence 5090, Appl

; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NH2-Phe
US-09-863-600E-38

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred No. 5, 8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
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Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 5
US-09-863-600E-39
; Sequence 39, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 39
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-NH2-Phe
US-09-863-600E-39

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred No. 5, 8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 6
US-09-863-600E-40
; Sequence 40, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis

; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-F-Phe
US-09-863-600E-40

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred No. 5, 8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 7
US-09-863-600E-41
; Sequence 41, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is p-I-Phe
US-09-863-600E-41

Query Match 96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred No. 5, 8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| ||||| |||||
Db 1 GGTXSCHFGPLTWCKPQGG 20

RESULT 8
US-09-863-600E-42
; Sequence 42, Application US/09863600E

```
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: Xaa is 3,5-dibromo-Tyr
US-09-863-600E-42

Query Match          96.7%; Score 119; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 5.8e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 9
US-09-858-935B-66
; Sequence 66, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaquié, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-66

Query Match          95.1%; Score 117; DB 11; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 10
US-09-863-600E-8

Query Match          95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 11
US-09-863-600E-30
; Sequence 30, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-30

Query Match          95.1%; Score 117; DB 12; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| ||||| ||||| |||||
Db 1 GGTASCHFGPLTWCKPQGG 20

RESULT 12
US-09-863-600E-32
; Sequence 32, Application US/09863600E
```

; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-863-600E-32

Query Match 91.1%; Score 112; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFPGPATWCKPQGG 20

RESULT 13
US-09-863-600E-33
; Sequence 33, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-863-600E-33

Query Match 91.1%; Score 112; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 5.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFPGPLAWCKPQGG 20

RESULT 14
US-09-863-600E-20
; Sequence 20, Application US/09863600E
; Publication No. US20030130197A1

; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-863-600E-20

Query Match 90.2%; Score 111; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 1 GGTYSCHFAPLTWCKPQGG 20

RESULT 15
US-09-863-600E-43
; Sequence 43, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Xaa is Ac-Gly
; US-09-863-600E-43

Query Match 90.2%; Score 111; DB 12; Length 20;
Best Local Similarity 94.7%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCKPQGG 20
||| ||||| ||||| |||||
Db 2 GTYSCHFGLTWCKPQGG 20

RESULT 16

```
US-09-863-600E-31
; Sequence 31, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-31
```

```
Query Match      88.6%; Score 109; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| |||| |||| |||| ||||
Db 1 GGTYSCHFGLTWCKPQGG 20
```

RESULT 17

```
US-09-863-600E-36
; Sequence 36, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-36
```

```
Query Match      88.6%; Score 109; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| |||| |||| |||| ||||
Db 1 GGTYSCHFGLTWCKAQGG 20
```

```
RESULT 18
US-09-863-600E-35
```

```
; Sequence 35, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-35
```

```
Query Match      87.0%; Score 107; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 GGTASCHFGPLTWCKPQGG 20
   ||| |||| |||| |||| ||||
Db 1 GGTYSCHFGLTFVCKPQGG 20
```

RESULT 19

```
US-09-863-600E-13
; Sequence 13, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-13
```

```
Query Match      85.4%; Score 105; DB 12; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.7e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 GGTASCHFGPLTWCKPQ 18
   ||| |||| |||| |||| |||
Db 1 GGTYSCHFGLTWCKPQ 18
```

```
RESULT 20
US-09-863-600E-22
; Sequence 22, Application US/09863600E
```

Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-22

Query Match 85.4%; Score 105; DB 12; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.7e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TASCDFGPLTWCKPQGG 20
| | | | | | | | | | | | | | | | | |
Db 1 TYSCHFGPLTWCKPQGG 18

RESULT 21
US-09-863-600E-34
; Sequence 34, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-34

Query Match 83.7%; Score 103; DB 12; Length 20;
Best Local Similarity 90.0%; Pred. No. 9.9e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTYSCHFGPLTAVCKPQGG 20

RESULT 22
US-09-863-600E-21
; Sequence 21, Application US/09863600E
; Publication No. US20030130197A1

GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-21

Query Match 80.1%; Score 98.5; DB 12; Length 19;
Best Local Similarity 90.0%; Pred. No. 4e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQGG 20
| | | | | | | | | | | | | | | | | |
Db 1 GGTYSCHFGPLTWCKPQGG 19

RESULT 23
US-09-863-600E-23
; Sequence 23, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-23

Query Match 75.6%; Score 93; DB 12; Length 16;
Best Local Similarity 93.8%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TASCDFGPLTWCKPQ 18
| | | | | | | | | | | | | | | | | |
Db 1 TYSCHFGPLTWCKPQ 16

RESULT 24
US-09-863-600E-46
; Sequence 46, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:

; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-46

Query Match 74.8%; Score 92; DB 12; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.4e-06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||||
Db 1 GGTYSRHFGPLTWCKPQGG 20

RESULT 25
US-09-863-600E-10
; Sequence 10, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-10

Query Match 72.4%; Score 89; DB 12; Length 20;
Best Local Similarity 68.4%; Pred. No. 8.8e-06;
Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCKPQGG 20
| ||||| |||||
Db 2 GNYMCHFGPITWCKPQGG 20

RESULT 26
US-09-863-600E-44
; Sequence 44, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia

; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-44

Query Match 72.4%; Score 89; DB 12; Length 20;
Best Local Similarity 65.0%; Pred. No. 8.8e-06;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||||
Db 1 GGLYACHMGPMTWVQPLGG 20

RESULT 27
US-09-863-600E-24
; Sequence 24, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-24

Query Match 69.1%; Score 85; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SCHFGPLTWCKP 17
||||| |||||
Db 2 SCHFGPLTWCKP 14

RESULT 28
US-09-863-600E-9
; Sequence 9, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael

; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-9

Query Match 69.1%; Score 85; DB 12; Length 20;
Best Local Similarity 70.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGDYHCRMGPITWVCKPLGG 20

RESULT 29

US-09-863-600E-45
; Sequence 45, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-45

Query Match 66.7%; Score 82; DB 12; Length 22;
Best Local Similarity 76.5%; Pred. No. 9.1e-05;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKP 17
Db 2 GRKYSCHFGPLTWVCQP 18

RESULT 30

US-09-863-600E-11
; Sequence 11, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos

; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-11

Query Match 65.9%; Score 81; DB 12; Length 20;
Best Local Similarity 60.0%; Pred. No. 0.00012;
Matches 12; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGVYACRMGPITWVCSPLGG 20

RESULT 31

US-09-863-600E-14
; Sequence 14, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-14

Query Match 65.9%; Score 81; DB 12; Length 20;
Best Local Similarity 60.0%; Pred. No. 0.00012;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGG 20
Db 1 GGLYACRMGPMTWVCPLRG 20

RESULT 32

US-09-863-600E-18
; Sequence 18, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda

```
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-863-600E-18
```

```
Query Match 63.4%; Score 78; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 SCHFGPLTWCK 16
Db 1 SCHFGPLTWCK 12
```

```
RESULT 33
US-10-271-343-14
; Sequence 14, Application US/10271343
; Publication No. US20030166003A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Skelton, Nicholas A.
; APPLICANT: Starcvasnik, Melissa A.
; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES
; TITLE OF INVENTION: ON PHAGE
; FILE REFERENCE: 11669.116US11
; CURRENT APPLICATION NUMBER: US/10/271,343
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/592,695
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/139,017
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Turn Peptide
; US-10-271-343-14
```

```
Query Match 63.4%; Score 78; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 SCHFGPLTWCK 16
Db 1 SCHFGPLTWCK 12
```

```
RESULT 34
US-09-863-600E-16
; Sequence 16, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
```

```
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-863-600E-16
```

```
Query Match 63.4%; Score 78; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 5 SCHFGPLTWCK 16
Db 2 SCHFGPLTWCK 13
```

```
RESULT 35
US-10-006-593-3
; Sequence 3, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: EPO mimetic peptide
; US-10-006-593-3
```

```
Query Match 62.6%; Score 77; DB 15; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.00038;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 6 CHFGPLTWCKPQG 20
Db 4 CRMGPLTWCKPLGG 18
```

```
RESULT 36
US-09-863-600E-25
; Sequence 25, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
```



```

; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-25

```

```

Query Match      59.3%; Score 73; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 SCHFGPLTWVC 15
Db      2 SCHFGPLTWVC 12

```

```

RESULT 37
US-09-863-600E-26
; Sequence 26, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-26

```

```

Query Match      56.9%; Score 70; DB 12; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0026;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      5 SCHFGPLTWVC 16
Db      2 SCHFGALTWVCK 13

```

```

RESULT 38
US-09-863-600E-17
; Sequence 17, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana

```

```

; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-17

```

```

Query Match      56.1%; Score 69; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 CHFGPLTWVC 15
Db      2 CHFGPLTWVC 11

```

```

RESULT 39
US-09-863-600E-12
; Sequence 12, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-12

```

```

Query Match      55.3%; Score 68; DB 12; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.0071;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      2 GTASCHFGPLTWVCKPQG 19
Db      2 GNYMAHMGPIITWVCRPGC 19

```

```

RESULT 40
US-09-863-600E-7
; Sequence 7, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides

```

FILE REFERENCE: PRI-0014 (ORT-1436)
CURRENT APPLICATION NUMBER: US/09/863,600E
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/207,654
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7
LENGTH: 20

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-7

Query Match 53.7%; Score 56; DB 12; Length 23;
Best Local Similarity 55.0%; Pred. No. 0.314; 7; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 7

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||
Db 1 GGLVLCRFGPTWDCGYKGG 20

RESULT 41

US-10-006-593-71
Sequence 71, Application US/10006593
Publication No. US20030049683A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES

FILE REFERENCE: 1087-2
CURRENT APPLICATION NUMBER: US/10/006,593
CURRENT FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/288,889
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 22

TYPE: PRT
ORGANISM: artificial sequence

FEATURE:
OTHER INFORMATION: EPO mimetic with random flanking amino acids

FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (1)..(2)
OTHER INFORMATION: Xaa is any amino acid

FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (6)..(6)
OTHER INFORMATION: Xaa is any amino acid

FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (15)..(15)
OTHER INFORMATION: Xaa is any amino acid

FEATURE:
NAME/KEY: MISC_FEATURE

LOCATION: (21)..(22)
OTHER INFORMATION: Xaa is any amino acid

US-10-006-593-71

Query Match 46.3%; Score 57; DB 15; Length 22;
Best Local Similarity 83.3%; Pred. No. 0.28;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 GPLTWCKPQGG 20

||||| ||| ||
Db 9 GPLTWCKPQGG 20

RESULT 42

US-09-863-600E-27
Sequence 27, Application US/09863600E
Publication No. US20030130197A1
GENERAL INFORMATION:

APPLICANT: Smith-Swintosky, Virginia

APPLICANT: Renzi, Michael

APPLICANT: Plata-Salaman, Carlos

APPLICANT: Jolliffe, Linda

APPLICANT: Farrell, Francis

APPLICANT: Johnson, Dana

TITLE OF INVENTION: Neuroprotective Peptides

FILE REFERENCE: PRI-0014 (ORT-1436)

CURRENT APPLICATION NUMBER: US/09/863,600E

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: 60/207,654

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn version 3.2

SEQ ID NO 27
LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Synthetic Peptide

US-09-863-600E-27

Query Match 43.9%; Score 54; DB 12; Length 14;
Best Local Similarity 55.0%; Pred. No. 0.48;
Matches 11; Conservative 1; Mismatches 2; Indels 6; Gaps 2;

Qy 1 GGTASCHFGPLTWCKPQGG 20
||| ||||| |||

Db 1 GGLVLCRFGPTWDCGYKGG 14

RESULT 43

US-09-858-935B-43
Sequence 43, Application US/09858935B

Publication No. US20030069177A1

GENERAL INFORMATION:

APPLICANT: Dubaqui, Yves

APPLICANT: Filvaroff, Ellen

APPLICANT: Lowman, Henry B.

TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS

FILE REFERENCE: P1794R1

CURRENT APPLICATION NUMBER: US/09/858,935B

CURRENT FILING DATE: 2002-07-02

PRIOR APPLICATION NUMBER: JS 60/248,985

PRIOR FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: US 60/204,490

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 153

SEQ ID NO 43
LENGTH: 21

TYPE: PRT
ORGANISM: Artificial sequence

FEATURE:
OTHER INFORMATION: Sequence is synthesized

US-09-858-935B-43

Query Match 43.1%; Score 53; DB 11; Length 21;
Best Local Similarity 53.3%; Pred. No. 0.96;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCK 16
||| ||||| |||

Db 1 GQOQCRAGPLQWLCE 15

RESULT 44
US-09-863-600E-15
; Sequence 15, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-15

Query Match 43.1%; Score 53; DB 12; Length 22;
Best Local Similarity 58.3%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 6 CHFGPLTWCKP 17
Db 7 CYNGPETWECSP 18
|: |||||:|

RESULT 45
US-09-863-600E-28
; Sequence 28, Application US/09863600E
; Publication No. US20030130197A1
; GENERAL INFORMATION:
; APPLICANT: Smith-Swintosky, Virginia
; APPLICANT: Renzi, Michael
; APPLICANT: Plata-Salaman, Carlos
; APPLICANT: Jolliffe, Linda
; APPLICANT: Farrell, Francis
; APPLICANT: Johnson, Dana
; TITLE OF INVENTION: Neuroprotective Peptides
; FILE REFERENCE: PRI-0014 (ORT-1436)
; CURRENT APPLICATION NUMBER: US/09/863,600E
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/207,654
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-863-600E-28

Query Match 41.5%; Score 51; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5, se-05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 HFGPLTW 14
Db 1 HFGPLTW 8
|||||||

RESULT 46
US-09-858-935B-153
; Sequence 153, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaigue, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 153
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-153

Query Match 41.5%; Score 51; DB 11; Length 21;
Best Local Similarity 53.3%; Pred. No. 1, 8;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GTASCHFGPLTWCK 16
Db 1 GQOSCAAGPLQWLCE 15
|: |||||:|

RESULT 47
US-09-858-935B-46
; Sequence 46, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubaigue, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 46
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-46

Query Match 41.5%; Score 51; DB 11; Length 23;
Best Local Similarity 53.3%; Pred. No. 2;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 GTASCHFGPLTWCK 16
Db 1 GQOSCAAGPLQWLCE 15
|: |||||:|

RESULT 48
US-09-858-935B-47
; Sequence 47, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:

APPLICANT: Dubaquié, Yves
APPLICANT: Flivartoff, Ellen
APPLICANT: Lowman, Henry B.
TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
FILE REFERENCE: PI794R1
CURRENT FILING DATE: 2002-07-02
CURRENT APPLICATION NUMBER: US 60/248,935B
PRIOR FILING DATE: 2000-11-15
PRIOR FILING DATE: 2000-11-15
PRIOR APPLICATION NUMBER: US 60/204,490
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 47
LENGTH: 97
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-47

Query Match 41.5%; Score 51; DB 1; Length 97;
Best Local Similarity 53.3%; Pred. No. 7.5;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GTASCHFGPLTWCK 16
Db : GQSCAAGPLQWLCE 15

RESULT 43

US-09-864-761-40377
Sequence 40377, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864, 761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/267,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 40377
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL132654.12
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EST_HUMAN HIT: A1208765.1, EVALUATE 9.00e-08
US-09-864-761-40377

Query Match 39.8%; Score 49; DB 9; Length 24;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 10; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 2 GTASC--HFGPLTWCKPOG 19
Db 2 GTSSCTARRGPLAWRTSPRG 21

RESULT 50

US-09-864-761-48118
Sequence 48118, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864, 761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/267,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48118
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010850.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
; OTHER INFORMATION: EST_HUMAN HIT: BF575401.1, EVALUE 5.40e+00
US-09-864-761-48118

```

```

Query Match          39.0%; Score 48; DB 9; Length 42;
Best Local Similarity 77.8%; Pred. No. 9.;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      10 PLTWCKPQ 18
Db      18 PLTWCSPR 26

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Search completed: November 5, 2003, 19:12:07
Job time : 30 secs

GenCore version 5.1.6
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OM: protein - protein search, using sw model

Run on: November 5, 2003, 19:03:58 ; Search time 21 Seconds
(without alignments)
91.589 Million cell updates/sec

Title: US-09-863-600E-19
Perfect score: 123
Sequence: 1 GGTASCHFGFLTWCKPQGG 20

Scoring table: B:OSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 76:*

1: piri:.*
2: piri2:.*
3: piri3:.*
4: piri4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	58	47.2	19	1 EWSMAN	anovenin - Strept
2	50.5	41.1	155	2 C69022	conserved hypotet
3	50	40.7	19	1 EWSMKN	cinnamycin - Strept
4	50	40.7	78	1 EWSMIG	cinnamycin precurs
5	49	39.8	499	2 S63465	dihydrolipoamide d
6	47	38.2	68	2 S36976	hypothetical prote
7	47	38.2	319	2 T47852	hypothetical prote
8	47	38.2	640	2 T29784	hypothetical prote
9	47	38.2	695	2 T52429	PM1 homolog (impo
10	46	37.4	240	2 S34619	probable fumarate
11	46	37.4	272	2 A12005	delta-9 desaturase
12	46	37.4	347	2 T33018	hypothetical prote
13	45.5	37.0	498	1 HJBBI1	helicase (EC 3.6.1
14	45	36.6	126	2 S54062	hypothetical prote
15	45	36.6	220	2 A12182	hypothetical prote
16	45	36.6	346	2 S34732	membrane protein -
17	45	36.6	370	2 C75268	carboxypeptidase G
18	45	36.6	1290	2 AE2192	two-component hybr
19	45	36.6	1622	2 D86428	glutathione S-conj
20	45	36.6	2910	2 T28156	DNA-directed RNA p
21	44	35.8	314	2 T17764	hypothetical prote
22	44	35.8	338	2 T49229	palmitoyl-protein
23	44	35.8	387	2 S46123	hypothetical prote
24	44	35.8	388	2 A83913	xylanase Y BH2105
25	44	35.8	522	1 KJHUG6	N-acetylglactosam
26	44	35.8	733	2 A97415	hypothetical prote
27	44	35.8	735	2 G02937	fertilin beta - cr
28	44	35.8	1539	2 S65775	homeotic protein H
29	43.5	35.4	437	2 S39069	vasoactive intesti

30	43	35.0	119	2	B98236	exs1 protein prote
31	43	35.0	123	2	S29714	guanine-nucleotide
32	43	35.0	123	2	S29714	guanine-nucleotide
33	43	35.0	199	2	A46711	probable thioether
34	43	35.0	356	2	T22998	hypothetical prote
35	43	35.0	397	2	T30088	hypothetical prote
36	43	35.0	483	2	A38560	nitrate transport
37	43	35.0	626	2	H82133	conserved hypotet
38	43	35.0	1520	2	T00273	hypothetical prote
39	42.5	34.6	96	2	E89273	hypothetical prote
40	42.5	34.6	347	2	S50403	Tif34 protein - ye
41	42	34.1	165	2	D84394	hypothetical prote
42	42	34.1	199	2	A48513	macrophage 23K str
43	42	34.1	199	2	A48513	hypothetical prote
44	42	34.1	288	2	B59405	probable thioether
45	42	34.1	347	2	T41373	prolactin receptor
46	42	34.1	376	2	A59405	hypothetical prote
47	42	34.1	426	2	A35641	prolactin receptor
48	42	34.1	554	2	E87375	5-aminoimidazole r
49	42	34.1	622	2	A40144	conserved hypotet
50	42	34.1	679	2	T00636	prolactin receptor
51	42	34.1	872	2	H86435	hypothetical prote
52	42	34.1	902	2	AD0587	protein Fl7F8_5 li
53	42	34.1	1506	2	T30886	sensor protein Kdp
54	41.5	33.7	60	2	A82662	integumentary muc
55	41.5	33.7	155	2	C64314	hypothetical prote
56	41.5	33.7	342	2	JT0370	conserved hypotet
57	41.5	33.7	982	1	GNLJH2	hypothetical prote
58	41.5	33.7	1133	1	GNVUSR	pol polyprotein -
59	41.5	33.7	1133	1	A43964	M polyprotein prec
60	41.5	33.7	1133	1	S12597	M polyprotein prec
61	41.5	33.7	1134	1	GNVU22	M polyprotein prec
62	41.5	33.7	1134	1	A43960	M polyprotein prec
63	41	33.3	128	2	T06028	hypothetical prote
64	41	33.3	197	2	A69201	rubrerythrin - Met
65	41	33.3	229	2	C71493	probable uracil DN
66	41	33.3	229	2	B81652	uracil-DNA glycosy
67	41	33.3	239	2	C81935	probable ribonucle
68	41	33.3	239	2	E81189	ribonuclease III N
69	41	33.3	248	2	D84242	sporulation protei
70	41	33.3	306	2	AE2685	conserved hypotet
71	41	33.3	306	2	G97466	homeotic cytochrome
72	41	33.3	330	2	A40855	homeotic protein H
73	41	33.3	338	2	D89102	protein F25E5_2 li
74	41	33.3	347	2	T20472	hypothetical prote
75	41	33.3	405	4	A61181	homeotic protein H
76	41	33.3	471	1	KR208	oryzain (EC 3.4.22
77	41	33.3	473	2	I49283	ADAM 4 protein pre
78	41	33.3	608	2	F83397	probable peptidase
79	41	33.3	650	2	B87466	TonB-dependent rec
80	41	33.3	756	2	G86150	F22M8_3 protein -
81	41	33.3	814	2	G02390	disintegrin-like m
82	41	33.3	873	1	I48952	VLDL receptor prec
83	41	33.3	906	2	G36621	probable disease f
84	40.5	32.9	290	2	F90154	SSV1 integrase hom
85	40.5	32.9	300	2	T52020	ethylene responsiv
86	40.5	32.9	437	2	JU0185	PACAP/VIP receptor
87	40.5	32.9	566	1	HMIVDU	hemagglutinin prec
88	40.5	32.9	1142	1	GNVUPH	M polyprotein prec
89	40.5	32.9	1225	2	T09395	envelope polyprote
90	40	32.5	771	1	I40863	piscicolin 61 prec
91	40	32.5	103	2	B2003	hypothetical prote
92	40	32.5	103	2	H86621	hypothetical prote
93	40	32.5	144	2	G86809	transcription regu
94	40	32.5	147	2	E82523	hypothetical prote
95	40	32.5	158	2	B82191	hypothetical prote
96	40	32.5	212	2	E64123	stringent starvari
97	40	32.5	244	2	T44604	beta-lactamase-lik
98	40	32.5	255	2	A11351	probable cobalt AB
99	40	32.5	316	2	D90585	hypothetical prote
100	40	32.5	331	2	D88986	protein C50H11.12

ALIGNMENTS

Db 61 GQGTG-FGLVMCKP 75

RESULT 1
EWSMAN
cinnamycin - Streptomyces sp. (strain A647p-2)
C:Species: Streptomyces sp.
C:Date: 12-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994
C:Accession: A61284
R:Naruse, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Motoaki, Y.
Tetrahedron Lett. 26, 665-668, 1985
A:Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I converting
A:Reference number: A61284
A:Accession: A61284
A:Molecule type: protein
A:Residues: 1-19 <WAK>
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6/Modified site: dehydroalanine (Ser) #status experimental

Query Match 47.2% Score 58; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.645;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCFPGPLTWVC 15
DB 4 SCSFGPLTWSC 14

RESULT 2
C69002
conserved hypothetical protein MTH10.4 - Methanobacterium thermoautotrophicum (strain De
N:Alternate names: orf2 atwA 3'-region
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999
C:Accession: C69002; C36921
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcu
A:Reference number: A69000; MUID:99037514; PMID:9371463
A:Accession: C69002
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-155 <MTH>
A:Cross-references: GB:A6000874; GB:A6000666; NID:g2622110; PIDN:AAB85510.1; PID:g262211
A:Experimental source: strain Delta H
R:Kühner, C.H.; Lindenbach, B.D.; Wolfe, R.S.
J. Bacteriol. 175, 3195-3203, 1993
A:Title: Component A2 of methylcoenzyme M reductase system from Methanobacterium thermo
A:Reference number: A36921; MUID:93259970; PMID:849734
A:Accession: C36921
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 32-66 <KUH>
A:Cross-references: GB:S61233; NID:g385922; PIDN:AAB26632.1; PID:g385925
A:Experimental source: strain Delta H
A:Note: sequence extracted from NCBI backbone (NCBIN:J32019, NCBI:P132022)
C:Genetics:
C:Gene: MTH1014
A:Start codon: TTG
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0115

Query Match 41.1% Score 50.5; DB 2; Length 155;
Best Local Similarity 56.2%; Pred. No. 3.7;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWCKP 17
: : | | | | | | |

RESULT 3
EWSMCN
cinnamycin - Streptovorticillium cinnamoneum
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium cinnamoneum
C:Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 07-May-1999
C:Accession: A45767
R:Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase,
J. Antibiot. 42, 837-845, 1989
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and propertie
A:Reference number: A45767; MUID:89291558; PMID:2544544
A:Accession: A45767
A:Molecule type: protein
A:Residues: 1-19 <NAR>
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structu
A:Reference number: A53359
A:Contents: annotation; strain L337-2
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:6-19/Cross-link: (2X1,9S)-lysinoalanine (Ser-Lys) #status experimental
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 40.7% Score 50; DB 1; Length 19;
Best Local Similarity 72.7%; Pred. No. 0.65;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCFPGPLTWVC 15
DB 4 SCSFGPTFVC 14

RESULT 4
EWSMYG
cinnamycin precursor - Streptovorticillium griseovorticillatum
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198
C:Species: Streptovorticillium griseovorticillatum
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C:Accession: S17181; A60555
R:Kaletta, C.; Entian, K.D.; Jung, G.
Eur. J. Biochem. 199, 411-415, 1991
A:Title: Prepeptide sequence of cinnamycin (Ro 09-0198): the first structural gene of
A:Reference number: S17181; MUID:91301152; PMID:2070795
A:Accession: S17181
A:Molecule type: DNA
A:Residues: 1-78 <KAL>
A:Cross-references: EMBL:X58545; NID:g47089; PIDN:CAA41436.1; PID:g47090
R:Kessler, H.; Steuernagel, S.; Will, M.; Jung, G.; Kellner, R.; Gillissen, D.; Kamf
Helv. Chim. Acta 71, 1924-1929, 1988
A:Title: The structure of the polycyclic nonadecapeptide Ro 09-0198.
A:Reference number: A60555
A:Accession: A60555
A:Molecule type: protein
A:Residues: 60-78 <KES>
C:Genetics:
C:Gene: cinA; rocA
C:Superfamily: cinnamycin precursor
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine
F:1-59/Domain: propeptide #status predicted <PRO>
F:60-78/Product: cinnamycin #status experimental <MAT>
F:63-73/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:63-73/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F:64-70/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F:65-78/Cross-link: (2X1,9S)-lysinoalanine (Ser-Lys) #status experimental
F:74/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

```

Query Match      40.7%; Score 50; DB 1; Length 78;
Best Local Similarity 72.7%; Pred. No. 2.4;
Matches      8; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

Qy      5 SCHFGPLTWVC 15
Db      63 SCSPGPTFTVC 73

RESULT 5
S63465
dihydrolipoamide dehydrogenase homolog YPL017c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein LPB14c
C:Species: Saccharomyces cerevisiae
C>Date: 16-May-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C:Accession: S63465
R:Wang, Y.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Hall, J.; Storms, R.K.; Vd
submitted to the EMBL Data Library, September 1995
A:Reference number: S63452
A:Accession: S63465
A:Molecule type: DNA
A:Residues: 1-499 <WAN>
A:Cross-references: EMBL:U36624; NID:g1276642; PID:AAB68170.1; PID:g1039460; GSPDB:GN00
C:Genetics:
A:Gene: MIPS:YPL017c
A:Cross-references: SGD:S0005938
A:Map position: 16L
A:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
F:21-479/Domain: dihydrolipoamide dehydrogenase homology <BLD>

Query Match      39.8%; Score 49; DB 2; Length 499;
Best Local Similarity 47.4%; Pred. No. 18;
Matches      9; Conservative      3; Mismatches      7; Indels      0; Gaps      0;

Qy      2 GTASCHFGPLTWCKPQGG 20
Db      361 GTSNCGPPPNVLYCQPIG 379

RESULT 6
S36976
hypothetical protein 10 - Synecchococcus sp. (PCC 6716)
C:Species: Synecchococcus sp.
A:Variety: PCC 6716
C>Date: 22-Jan-1994 #sequence_revision 12-Apr-1996 #text_change 08-Oct-1999
C:Accession: S36976; S31900
R:van Walraven, H.S.; Lutter, R.; Walker, J.E.
Biochem. J. 294, 239-251, 1993
A:Title: Organization and sequences of genes for the subunits of ATP synthase in the
A:Reference number: S36960; MUID:93371369; PMID:8363578
A:Accession: S36976
A:Molecule type: DNA
A:Residues: 1-68 <VAN>
A:Cross-references: EMBL:X70432; NID:g49226; PID:CAA49886.1; PID:g49231
A:Experimental source: PCC 6716

Query Match      38.2%; Score 47; DB 2; Length 68;
Best Local Similarity 50.0%; Pred. No. 5.7;
Matches      8; Conservative      2; Mismatches      6; Indels      0; Gaps      0;

Qy      2 GTASCHFGPLTWCKP 17
Db      8 GNSMSMTGPTITWIKP 23

RESULT 7
T47852
hypothetical protein T8B10.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47852
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, March 2000

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A:Reference number: Z24478
A:Accession: T47852
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <RIE>
A:Cross-references: EMBL:AL138646
A:Experimental source: cultivar Columbia; BAC clone T8B10
C:Genetics:
A:Map position: 3
A:Introns: 297/3
A>Note: T8B10.70

Query Match      38.2%; Score 47; DB 2; Length 319;
Best Local Similarity 44.4%; Pred. No. 23;
Matches      8; Conservative      3; Mismatches      7; Indels      0; Gaps      0;

Qy      1 GGTASCHFGPLTWCKPQ 18
Db      183 GGQEADEFQPKTNLRPR 200

RESULT 8
T29784
hypothetical protein F31F7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29784
R:Ledwith, J.; Wohlmann, P.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid F31F7.
A:Reference number: Z20695
A:Accession: T29784
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-640 <LED>
A:Cross-references: EMBL:U97011; PIDN:AAB52325.1; GSPDB:GN00023; CESP:F31F7.2
A:Experimental source: strain Bristol N2; clone F31F7
C:Genetics:
A:Gene: CESP:F31F7.2
A:Map position: 5
A:Introns: 115/3; 203/3; 266/1; 305/1; 411/3; 508/3; 527/3; 614/1

Query Match      38.2%; Score 47; DB 2; Length 640;
Best Local Similarity 53.8%; Pred. No. 43;
Matches      7; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

Qy      2 GTASCHFGPLTWV 14
Db      266 GSSSTRFQPLCW 278

RESULT 9
T52429
PRM1 homolog [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C:Accession: T52429
R:Kato, A.; Suzuki, M.; Kuwahara, A.; Coe, H.; Higano-Inaba, K.; Kameda, Y.
Gene 239, 309-316, 1999
A:Title: Isolation and analysis of cDNA within a 300 kb Arabidopsis thaliana genomic
A:Reference number: Z25171
A:Accession: T52429
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-695 <KAT>
A:Cross-references: EMBL:AB028231; PIDN:BAA87956.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: CW9
A:Map position: 1

Query Match      38.2%; Score 47; DB 2; Length 695;
Best Local Similarity 50.0%; Pred. No. 47;

```


Matches 8; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 3 TASCHFGPLTWCKPQ 18
 Db 185 TVRSHFAQLAWCVSQ 200

RESULT 10

S34619
 Probable fumarate reductase (EC 1.3.99.1) iron-sulfur protein - Thermoplasma acidophilum
 C:Species: Thermoplasma acidophilum
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S34619
 R:Bach, M.; Reilaender, H.; Gaertner, P.; Lottspeich, F.; Michel, H.
 Biochim. Biophys. Acta 1174, 103-107, 1993
 A:Title: Nucleotide sequence of a putative succinate dehydrogenase operon in Thermoplasma
 A:Reference number: S34619; MUID:93326626; PMID:8334158
 A:Accession: S34619
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <BAC>
 A:Cross-references: EMBL:X70908; NID:g396211; PID:g396212
 C:Superfamily: fumarate reductase iron-sulfur protein; ferredoxin 2[4Fe-4S] homology; ferredoxin 2[4Fe-4S]; 3Fe-4S; 4Fe-4S; iron-sulfur protein; metalloprotein; oxidoreductase
 F:33-75/Domain: ferredoxin [2Fe-2S] homology <FER1>
 F:139-220/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
 F:54-59,62,74/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted
 F:146,149,152,212/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:156,202,208/Binding site: 3Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 37.4%; Score 46; DB 2; Length 240;
 Best Local Similarity 57.9%; Pred. No. 25;
 Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

Qy 2 GTASCHFGPLTWCKPQ 19
 Db :98 GTSRCHPAGECTEVC-PAG 215

RESULT 11

AI2005
 delta-9 desaturase [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C:Accession: AI2005
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AI2005
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-272 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA077965.1; PID:g17135419; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: desc
 C:Superfamily: mammalian stearyl-CoA desaturase; stearyl-CoA desaturase homology

Query Match 37.4%; Score 46; DB 2; Length 272;
 Best Local Similarity 53.8%; Pred. No. 28;
 Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

Qy 2 GTASCHFGPLTWV 14
 Db 82 GTLACQCGPIEW 94

RESULT 12

T33018
 hypothetical protein K07H8.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T33018
 R:Fulton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.
 submitted to the EMBL Data Library, February 1998
 A:Description: The sequence of C. elegans cosmid K07H8.
 A:Reference number: Z21264
 A:Accession: T33018
 A:Status: preliminary; translated from GB/EMBL/DD8J
 A:Molecule type: DNA
 A:Residues: 1-347 <FUL>
 A:Cross-references: EMBL:AF047659; PIDN:AAC04429.1; GSPDB:GN00022; CESP:K07H8.8
 A:Experimental source: strain Bristol N2; clone K07H8
 C:Genetics:
 A:Gene: CESP:K07H8.8
 A:Map position: 4
 A:Introns: 47/1; 110/3; 158/2; 202/2; 249/2; 302/1

Query Match 37.4%; Score 46; DB 2; Length 347;
 Best Local Similarity 58.3%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ASCHFGPLTWVC 15
 Db 240 ADTHFAPQTWYC 251

RESULT 13

KJBE11
 helicase (EC 3.6.1.-) - ictalurid herpesvirus 1 (strain auburn 1)
 C:Species: ictalurid herpesvirus 1
 A:Note: host ictalurid punctatus (channel catfish)
 C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
 C:Accession: H36788
 R:Davidson, A.J.
 submitted to GenBank, January 1992
 A:Description: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A36804
 A:Accession: H36788
 A:Molecule type: DNA
 A:Residues: 1-498 <DAV>
 A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA88128.1; PID:g331235
 R:Davidson, A.J.
 Virology 186, 9-14, 1992
 A:Title: Channel catfish virus: a new type of herpesvirus.
 A:Reference number: A39447; MUID:92087490; PMID:1727613
 A:Contents: annotation
 A:Note: neither amino acid nor nucleotide sequence is given
 C:Genetics:
 A:Gene: 25
 C:Superfamily: ictalurid herpesvirus helicase
 C:Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding; 3'-44/Region: nucleotide-binding motif A (p-loop)

Query Match 37.0%; Score 45.5; DB 1; Length 498;
 Best Local Similarity 56.2%; Pred. No. 57;
 Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GGTASCHFGPL-TWVC 15
 Db 323 GGSASCRFGALIEYMC 338

RESULT 14

S54062
 hypothetical protein YML122c - yeast (Saccharomyces cerevisiae)
 A:Alternate names: hypothetical protein YM7056.04c
 C:Species: Saccharomyces cerevisiae
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S54062
 R:Badcock, K.; Churcher, C.M.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54059

ansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khar, S.; Khaykin, E.; Kim, C.
 C:Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Pizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, X.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:1130712
 A:Accession: D86428
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1622 <STO>
 A:Cross-references: GB:AE005172; NID:gill355814; PION:AAG28284.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1
 C:Superfamily: human multidrug resistance protein: cMOAT2; ATP-binding cassette homology

Query Match 36.6%; Score 45; DB 2; Length 1622;
 Best Local Similarity 70.0%; Pred. No. 2e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 FGPLTWCKP 17
 DB 3 FEPDWCKP 12

RESULT 20
 T28156
 DNA-directed RNA polymerase homolog - malaria parasite (Plasmodium falciparum)
 C:Species: Plasmodium falciparum
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
 C:Accession: T28156
 R:Fox, B.A.; Li, W.B.; Tanaka, M.; Inselburg, J.; Bzik, D.J.
 Mol. Biochem. Parasitol. 61, 37-48, 1993
 A:Title: Molecular characterization of the largest subunit of plasmodium falciparum RNA
 A:Reference number: Z20478; MUID:94091864; PMID:8259131
 A:Accession: T28156
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-2910 <FOX>
 A:Cross-references: EMBL:L11172; NID:g414321; PID:g414322; PION:AAA72349.1
 C:Genetics:
 A:Introns: 2840/3; 2880/1

Query Match 36.6%; Score 45; DB 2; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 HFGPLTWCK 16
 DB 2702 HFGPVTWCK 2711

RESULT 21
 T17764
 hypothetical protein A267L - Chlorella virus PBCV-1
 C:Species: Chlorella virus PBCV-1
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17764
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: Z18806
 A:Accession: T17764
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-314 <GRA>
 A:Cross-references: EMBL:U42580; NID:g4028896; PION:AAC96635.1
 A:Experimental source: specific host Chlorella strain NC64A
 C:Genetics:
 A:Note: A267L

Query Match 35.8%; Score 44; DB 2; Length 314;

Best Local Similarity 53.8%; Pred. No. 62;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTW 13
 DB 188 GCAICHRRAPITW 200

RESULT 22
 T49229
 palmitoyl-protein thioesterase-like protein F27H5.130 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
 C:Accession: T49229
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25018
 A:Accession: T49229
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-338 <RIE>
 A:Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.130
 A:Experimental source: cultivar Columbia; BAC clone F27H5
 C:Genetics:
 A:Gene: ATSP:F27H5.130
 A:Map position: 3
 A:Introns: 30/1; 58/2; 75/3; 82/3; 117/3; 138/3; 160/3; 173/3; 213/3; 244/3

Query Match 35.8%; Score 44; DB 2; Length 338;
 Best Local Similarity 57.1%; Pred. No. 66;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWVC 15
 DB 130 GTASIFPCGATWIC 143

RESULT 23
 S46123
 hypothetical protein YBR246w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein YBR1634
 C:Species: Saccharomyces cerevisiae
 C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
 C:Accession: S46123
 R:Aljinovic, G.; Pohl, F.M.; Pohl, T.M.
 submitted to the Protein Sequence Database, August 1994
 A:Reference number: S45906
 A:Accession: S46123
 A:Molecule type: DNA
 A:Residues: 1-387 <ALJ>
 A:Cross-references: EMBL:Z36115; NID:g536658; GSPDB:GN00002; MIPS:YBR246
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: MIPS:YBR246w
 A:Cross-references: SGD:S0000450
 A:Map position: 2R

Query Match 35.8%; Score 44; DB 2; Length 387;
 Best Local Similarity 69.2%; Pred. No. 75;
 Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 4 ASCHFGPLTWCK 16
 DB 125 ASCHFSPLD--CK 135

RESULT 24
 A83913
 xylanase Y BH2105 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: A83913
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; F

Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: A83913
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-388 <STO>
 A:Cross-references: GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BA05824.1; GSPDB:GN000
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH2105

Query Match 35.8%; Score 44; DB 2; Length 388;
 Best Local Similarity 41.2%; Pred. No. 75;
 Matches 7; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQG 19
 Db 102 TEGVHAGYFAWSCQPDG 118

RESULT 25
 KJHUG6
 N-acetylglucosamine-6-sulfatase [EC 3.1.6.4] precursor [validated] - human
 N:Alternate names: chondroitinase; chondroitinsulfatase; galactose-6-sulfate sulfatase;
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1992 #sequence revision 27-Oct-1995 #text_change 08-Dec-2000
 C:Accession: JQ1299; PQ0242; I37406
 R:Tomatsu, S.; Fukuda, S.; Masue, M.; Sukegawa, K.; Fukao, T.; Yamagishi, A.; Hori, T.;
 ashi, Y.; Orii, T.
 Biochem. Biophys. Res. Commun. 181, 677-683, 1991

A:Title: Morquio disease: isolation, characterization and expression of full-length cDNA
 A:Reference number: JQ1299; MUID:92095973; PMID:1755950
 A:Accession: JQ1299
 A:Molecule type: mRNA
 A:Residues: 1-522 <TCM>
 A:Experimental source: placenta
 A:Accession: PQ0242

A:Molecule type: protein
 A:Residues: 27-42, 'X', 44-54, 175-183, 'X', 185-192; 201-218; 243-265; 311-324, 'XX', 327-336; 377
 R:Morris, C.P.; Guo, X.H.; Apostolou, S.; Hopwood, J.J.; Scott, H.S.
 Genomics 22, 652-654, 1994

A:Title: Morquio A syndrome: cloning, sequence, and structure of the human N-acetylgluc
 A:Reference number: I37406; MUID:95095267; PMID:8001980

A:Accession: I37406
 A:Status: preliminary; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-522 <RES>
 A:Note: nucleotide sequence not complete

C:Genetics:
 A:Gene: GDB:GALNS
 A:Cross-references: GDB:129085; OMIM:253000
 A:Map position: 16q24-16q24
 A:Introns: 40/3; 82/1; 107/1; 141/2; 189/2; 211/3; 253/2; 300/1; 334/3; 380/2; 414/3; 45
 A:Note: defects in this gene can cause mucopolysaccharidosis type IV A, Morquio disease

C:Function:
 A:Description: hydrolyzes N-acetylglucosamine-6-sulfate units in chondroitin sulfate a
 C:Superfamily: animal sulfatase
 C:Keywords: glycoprotein; sulfuric ester hydrolase
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-522/Product: N-acetylglucosamine-6-sulfatase #status experimental <MAT>
 F:79/Modified site: 3-oxoalanine (Cys) #status predicted
 F:204,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.8%; Score 44; DB 1; Length 522;
 Best Local Similarity 43.8%; Pred. No. 98;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
 Db 16: GSPNCHFGPYDNKARP 176

RESULT 26

A97415
 hypothetical protein AGR_C_812 [imported] - Agrobacterium tumefaciens (strain C58, Ce
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 C:Accession: A97415
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldm
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
 A:Reference number: A97559; MUID:21608551; PMID:11743194

A:Accession: A97415
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-733 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK86274.1; PID:g15155384; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_812
 A:Map position: circular chromosome

Query Match 35.8%; Score 44; DB 2; Length 733;
 Best Local Similarity 46.2%; Pred. No. 1.3e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 8 FGPLTWCKPQGG 20
 Db 348 YGPTQWACENQAG 360

RESULT 27

G02937
 ferritin beta - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000
 C:Accession: G02937; S55061
 R:Ramatao, C.S.; Myles, D.G.; White, J.M.; Primakoff, P.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: G12615

A:Accession: G02937
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-735 <RAM>

A:Cross-references: EMBL:U33959; NID:g998339; PID:g998340
 R:Perry, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.

Biochem. J. 307, 843-850, 1995
 A:Title: Cloning and analysis of monkey ferritin reveals novel alpha subunit isoforms
 A:Reference number: S55059; MUID:95260313; PMID:7741716

A:Accession: S55061
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-722, 'S', 724-735 <PER>
 A:Cross-references: EMBL:X77653; NID:g794076; PIDN:CAAS4733.1; PID:g794077
 C:Superfamily: mouse meltrin alpha; disintegrin homology
 F:383-468/Domain: disintegrin homology <Dis>

Query Match 35.8%; Score 44; DB 2; Length 735;
 Best Local Similarity 44.0%; Pred. No. 1.3e+02;
 Matches 11; Conservative 1; Mismatches 3; Indels 10; Gaps 2;

QY 1 GGTASC---HF-----GPLTWVC 15
 Db 460 GTSASCPENHFQTGHPGCPGNQWVC 484

RESULT 28

S65775
 homeotic protein Hox2b - maize
 C:Species: Zea mays (maize)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 11-Jan-2002
 C:Accession: S65775; S72455
 R:Klinge, B.; Ueberlacker, B.; Korfhaage, C.; Merr, W.
 Plant Mol. Biol. 30, 439-453, 1996

A:Title: Z-Hox: a novel class of maize homeobox genes.
A:Reference number: S65774; MUID:96189260; PMID:8605297
A:Accession: S65775
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1539 <KLI>
A:Cross-references: EMBL:X89761
R:Wett, W.
submitted to the EMBL Data Library, July 1995
A:Reference number: S72455
A:Accession: S72455
A:Molecule type: mRNA
A>Status: preliminary
A:Residues: 1-379, 'S', 381-1539 <WER>
A:Cross-references: EMBL:X89761; NID:g1143706; PIDN:CAA61910.1; PID:g1143707
C:Genetics:
C:Superfamily: unassigned homeobox proteins; homeobox homology
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation
F:902-858/Domain: homeobox homology <HOX1>
F:1040-1096/Domain: homeobox homology <HOX2>

Query Match 35.8%; Score 44; DB 2; Length 1539;
Best Local Similarity 54.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTASCHFGPL 11
| : |||||
DB 1039 GDASKCHFGPI 1049

RESULT 29
S19069
vasoactive intestinal peptide receptor VIP2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 07-Oct-1994 #sequence_revision 10 Nov-1995 #text_change 08-Oct-1999
C:Accession: S19069
R:Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.
FEBS Lett. 314, 3-8, 1993
A:Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel receptor
A:Reference number: S19069; MUID:94039806; PMID:8224221
A:Accession: S19069
A:Molecule type: mRNA
A:Residues: 1-437 <LUT>
A:Cross-references: EMBL:Z25885; NID:9414188; PIDN:CAA81104.1; PID:9414189
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 35.4%; Score 43; DB 2; Length 437;
Best Local Similarity 56.2%; Pred. No. 99;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTW-CK 16
| : |||||
DB :87 GTLRCHDQPGSWVGCK 202

RESULT 30
B98236
exs1 protein protein (AJ225561) (imported) - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: B98236
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blarchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Woilam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B98236
A:Molecule type: DNA
A:Residues: 1-119 <KUR>
A:Cross-references: GB:AE008780; PIDN:AAK89412.1; PID:g15:59269; GSPCB:GN00170

C:Genetics:
A:Gene: AGR_L1677
A:Map position: linear chromosome

Query Match 35.0%; Score 43; DB 2; Length 119;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 FGPLTWCKP 17
| : |||||
DB 23 FGPAFLCRP 32

RESULT 31
S29714
guanine-nucleotide-releasing protein mss4 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S29714
R:Burton, J.; Roberts, D.; Montaldi, M.; Novick, P.; de Camilli, P.
Nature 361, 464-467, 1993
A:Title: A mammalian guanine-nucleotide-releasing protein enhances function of yeast
A:Reference number: S29714; MUID:93156814; PMID:8429887
A:Accession: S29714
A:Molecule type: mRNA
A:Residues: 1-123 <BUR>
A:Cross-references: EMBL:X70496; NID:g31387.1; PIDN:CAA49904.1; PID:g313872
C:Genetics:
A:Gene: mss4

Query Match 35.0%; Score 43; DB 2; Length 123;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
| : |||||
DB 95 ADCEIGPIGWHC 106

RESULT 32
I52427
guanine-nucleotide-releasing protein Mss4 - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I52427
R:Yu, H.; Schreiber, S.L.
Biochemistry 34, 9103-9110, 1995
A:Title: Cloning, Zn2+ binding, and structural characterization of the guanine nucle
A:Reference number: I52427; MUID:95345082; PMID:7619808
A:Accession: I52427
A:Molecule type: mRNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-123 <RES>
A:Cross-references: GB:S78873; NID:g1037135; PIDN:AAB34955.1; PID:g1037136
C:Genetics:
A:Gene: GDB:MSS4
A:Cross-references: GDB:683578

Query Match 35.0%; Score 43; DB 2; Length 123;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
| : |||||
DB 95 ADCEIGPIGWHC 106

RESULT 33
A46711
probable thioredoxin peroxidase (EC 1.11.1.1) PAGA - human
N:Alternate names: enhancer protein; heme-binding 23K protein (HBP23); natural kille
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000

C;Accession: A46711; I54533; S32099
 R;Prosperi, M.T.; Ferbus, D.; Karczynski, I.; Goubin, G.
 J. Biol. Chem. 269, 11050-11056, 1993
 A;Title: A human cDNA corresponding to a gene overexpressed during cell proliferation en
 A;Reference number: A46711; MUID:93266552; PMID:8496166
 A;Accession: A46711
 A;Molecule type: mRNA
 A;Residues: 1-199 <PRO>
 A;Cross-references: EMBL:X67951; NID:Q287640; PIDN:CAA48137.1; PID:Q287641
 A;Experimental source: ras-transformed mammary epithelial cell line HBL100
 A;Note: sequence extracted from NCBI backbone (NCBI:P132800)
 R;Shau, H.; Butterfield, L.H.; Chiu, R.; Kim, A.
 Immunogenetics 40, 129-134, 1994
 A;Title: Cloning and sequence analysis of candidate human natural killer-enhancing facto
 A;Reference number: I54533; MUID:94299283; PMID:8026862
 A;Accession: I54533
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-146, 'P', 148, 'CC', 151-188, 'P', 190, 'T', 192-199 <SHA>
 A;Cross-references: GB:L19184; NID:G440305; PIDN:AAA50464.1; PID:G440306
 C;Genetics:
 A;Gene: GDB:PAGA
 A;Cross-references: GDB:230262; OMIM:176763
 A;Map position: ip34.1-1p34.1
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 pro
 C;Keywords: here; oxidoreductase
 F;15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>
 Query Match 35.0%; Score 43; DB 2; Length 199;
 Best Local Similarity 45.5%; Pred. No. 57;
 Matches 10; Conservative 1; Mismatches 9; Indels 2; Gaps 1;
 Cy 1 GGTASCHFGPLTWCKP--QGG 20
 | | | | | | | | | |
 Db 75 GASVDSHFCHLAWNTPKQGG 96
 |||||
 RESULT 34
 T22998
 Hypothetical protein F59D12.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C;Accession: T22998
 R;Lloyd, C.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19649
 A;Accession: T22998
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-356 <WIL>
 A;Cross-references: EMBL:Z81558; PIDN:CAR04541.1; GSPDB:GN00028; CESP:F59D12.3
 A;Experimental source: clone F59D12
 C;Genetics:
 A;Gene: CESP:F59D12.3
 A;Map position: X
 A;Introns: 40/1; 111/3; 158/2; 202/2; 252/2; 306/1
 Query Match 35.0%; Score 43; DB 2; Length 356;
 Best Local Similarity 55.6%; Pred. No. 97;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Cy 7 HFGLTWVC 15
 | | | | |
 Db 246 HFAPMSWFC 254
 |||||
 RESULT 35
 T30088
 Hypothetical protein AH9.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T30088
 R;Stallies, L.; Gattung, S.

submitted to the EMBL Data Library, November 1995
 A;Description: The sequence of C. elegans cosmid AH9.
 A;Reference number: Z20733
 A;Accession: T30088
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-397 <STE>
 A;Cross-references: EMBL:U41270; PIDN:AAAB2442.1; CESP:AH9.4
 C;Genetics:
 A;Gene: CESP:AH9.4
 A;Introns: 63/3; 150/1; 166/2; 204/3; 290/3; 348/1
 Query Match 35.0%; Score 43; DB 2; Length 397;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
 Cy 1 GGTASCHFGPLTWCKPQ 18
 | | | | | | | | | |
 Db 74 GITAGCHVGELVLLSKAQ 91
 |||||
 RESULT 36
 A38560
 Nitrate transport protein crnA - Emericella nidulans
 C;Species: Emericella nidulans, Aspergillus nidulans
 C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 17-Mar-2000
 C;Accession: A38560
 R;Unkles, S.E.; Hawker, K.L.; Griewe, C.; Campbell, E.I.; Montague, P.; Kinghorn, J.R.
 Proc. Natl. Acad. Sci. U.S.A. 88, 204-208, 1991
 A;Title: crnA encodes a nitrate transporter in Aspergillus nidulans.
 A;Reference number: A38560; MUID:91095428; PMID:1986367
 A;Accession: A38560
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-483 <UNK>
 A;Cross-references: GB:M57647
 C;Superfamily: nitrate transporter component
 C;Keywords: transmembrane protein
 Query Match 35.0%; Score 43; DB 2; Length 483;
 Best Local Similarity 47.4%; Pred. No. 1.3e+02;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 Cy 2 GTASCHFGPLTWCKPQGG 20
 | | | | | | | | | |
 Db 354 GRWAAMFGFLNIVCRPAGG 372
 |||||
 RESULT 37
 H82133
 conserved hypothetical protein VC1966 [imported] - Vibrio cholerae (strain N16961 ser
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: H82133
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bae, S.; Qin, H.; Dragoi, I.; Sellers
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: H82133
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-626 <HEI>
 A;Cross-references: GB:AE004272; GB:AE003852; NID:G9655504; PIDN:AAF95114.1; GSPDB:GN
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC1966
 A;Map position: 1
 Query Match 35.0%; Score 43; DB 2; Length 626;
 Best Local Similarity 47.1%; Pred. No. 1.6e+02;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKPQ 18
 ||| ||| ||| |||
 Db 123 GTQSAFFGVYALLPQ 139

RESULT 38

T00273
 Hypothetical protein KIA0595 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
 C:Accession: T00273
 C:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A:Title: Prediction of the coding sequences of unidentified human genes. IX. The complete
 A:Reference number: 214086; MUID:98293545; PMID:9628581
 A:Accession: T00273
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1520 <NAG>
 A:Cross-references: EMBL:AB011167; NID:G3043713; PIDN:BAA25521.1; PID:G3043714
 A:Experimental source: brain
 C:Genetics:
 A:Note: KIA0595

Query Match 35.0% Score 43; DB 2; Length 1520;
 Best Local Similarity 43.8% Pred. No. 3.6e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 3 TASCHFGPLTWCKPQ 18
 ||| ||| ||| |||
 Db 810 SSTCYGPGTGMGGPQ 845

RESULT 39

E69273
 Hypothetical protein AF0189 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: E69273
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 : Fleischmann, R.D.; Ockenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: E69273
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-96 <KLS>
 A:Cross-references: GB:AE001093; GB:AE000782; NID:G2689416; PIDN:AA891047.1; PID:G265045

Query Match 34.6% Score 42.5; DB 2; Length 96;
 Best Local Similarity 70.0% Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 6 CHFGPLTWVC 15
 ||| ||| |||
 Db 50 CHFRP-SWVC 58

RESULT 40

S50403
 TIF34 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YN9375.16c; protein YMR146C
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 24-Sep-1999
 C:Accession: S50403
 R:Badcock, K.; Churcher, C.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S50388

A:Accession: S50403
 A:Molecule type: DNA
 A:Residues: 1-347 <BAD>
 A:Cross-references: EMBL:Z47071; NID:G606429; PIDN:CAA87361.1; PID:G606445; MIPS:YMR1
 C:Genetics:
 A:Gene: SGD:TIF34
 A:Cross-references: SGD:S0004754; MIPS:YMR146C
 A:Map position: 13R
 C:Superfamily: TGF-beta receptor interacting protein; WD repeat homology

Query Match 34.6% Score 42.5; DB 2; Length 347;
 Best Local Similarity 52.6% Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 2 GTASCHFGPLTWVC-KPOG 19
 ||| ||| ||| |||
 Db 287 GRVGHFGPLNTVAISPOG 305

RESULT 41

D84394
 Hypothetical protein Vng2439h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: D84394
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
 : Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jc
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbardt, H.; Lowe, T.M.,
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: D84394
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165 <STO>
 A:Cross-references: GB:AE004437; NID:G10581842; PIDN:AAG20520.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: VNG2439H

Query Match 34.1% Score 42; DB 2; Length 165;
 Best Local Similarity 62.5% Pred. No. 67;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 13 WVCKPQGG 20
 ||| ||| |||
 Db 105 WACEPEGG 112

RESULT 42

A48513
 Macrophage 23K stress-induced protein - mouse
 N:Alternate names: MSP23; osteoblast specific factor 3
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Jun-2000
 C:Accession: A48513; J02259
 R:Ikshii, T.; Yamada, M.; Sato, H.; Matsue, M.; Taketani, S.; Nakayama, K.; Sugita, Y
 J. Biol. Chem. 268, 18633-18636, 1993
 A:Title: Cloning and characterization of a 23-kDa stress-induced mouse peritoneal mac
 A:Reference number: A48513; MUID:93366771; PMID:8360158
 A:Accession: A48513
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-199 <ISH>
 A:Cross-references: GB:D16142; NID:G286102; PIDN:BAA03713.1; PID:G303690
 A:Experimental source: peritoneal macrophages
 A:Note: authors translated the codon TGG for residue 177 as Thr, and CAG for residue
 A:Note: authors suggest a role in an oxidoreductase reaction system in mammalian cel
 R:Kawai, S.; Takehita, S.; Okazaki, M.; Kikuno, R.; Kudo, A.; Amann, E.
 J. Biochem. 115, 641-643, 1994
 A:Title: Cloning and characterization of OSF-3, a new member of the MERS family, exp
 A:Reference number: J02259; MUID:94375405; PMID:8089076
 A:Accession: J02259

A:Molecule type: mRNA
A:Residues: 1-199 <RAW>
A:Cross-references: DDBJ:D21252; NID:G666969; PIDN:BAA04796.1; PID:G666970
A:Experimental source: osteoblastic cell line MC3T3-E1
A:Note: authors suggest, on the basis of homology to MER5 family, that this protein plays a role in cytokine receptor signaling
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C22 protein
C:Keywords: glycoprotein
F:1-157/Domain: alkyl hydroperoxidase C22 protein homology <C22>
F:157-199/Domain: alkyl hydroperoxidase C22 protein homology <C22>
F:199/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 199;
Best Local Similarity 40.9%; Pred. No. 80;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 GGTASCHFGPLTWCKP--QGG 20
DB 75 GASVDSHFCHLAWINTPKKQGG 96

RESULT 43
I52425
probable thioredoxin peroxidase (EC 1.11.1.1) HBP23 - rat
N:Alternate names: heme-binding 23K protein (HBP23); proliferation associated protein P
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Jun-2000
C:Accession: I52425
R:Iwahata, S.
Biochemistry 34, 13398-13406, 1995
A:Title: Purification, characterization, and cloning of a heme-binding protein (23 kDa)
A:Reference number: I52425; MUID:96027454; PMID:7577926
A:Accession: I52425
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-199 <RAW>
A:Cross-references: GB:D30035; NID:G1060976; PIDN:BAA06275.1; PID:G1060977
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C22 protein
C:Keywords: heme; oxidoreductase
F:1-157/Domain: alkyl hydroperoxidase C22 protein homology <C22>

Query Match 34.1%; Score 42; DB 2; Length 199;
Best Local Similarity 40.9%; Pred. No. 80;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 1 GGTASCHFGPLTWCKP--QGG 20
DB 75 GASVDSHFCHLAWINTPKKQGG 96

RESULT 44
B59405
prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C:Accession: B59405; B49400
R:Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin receptor
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: B59405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <HUI>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
R:Hu, Z.Z.
submitted to GenBank, December, 1999
A:Reference number: A49400
A:Accession: B49400
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-288 <HUI>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor gene promoter activation, with S1b more effective than S1a. However, their

C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
F:15-221/Domain: cytokine receptor homology <CRS>
F:59,104,213/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 288;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
DB 81 GGPNSCHFG 89

RESULT 45
T41373
hypothetical protein SPCC4G3.03 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41373
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: 221918
A:Accession: T41373
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-347 <WOO>
A:Cross-references: EMBL:Z97052; PIDN:CAB09780.1; GSPDB:GND0068; SPDB:SPCC4G3.03
C:Experimental source: strain 972h-; cosmid c4G3
C:Genetics:
A:Gene: SPDB:SPCC4G3.03
A:Map position: 3

Query Match 34.1%; Score 42; DB 2; Length 347;
Best Local Similarity 45.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 1 GGTASCHFGPLTWCKPQGG 20
DB 252 GSIRSCHFTP-----PNOG 265

RESULT 46
A59405
prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 23-Sep-2002
C:Accession: A59405; A49400
R:Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin receptor
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: A59405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HUI>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
R:Hu, Z.Z.
submitted to GenBank, December, 1999
A:Reference number: A49400
A:Accession: A49400
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HUI>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
C:Comment: This is one of the short forms (S1a and S1b) of the human prolactin receptor gene promoter activation, with S1a less effective than S1b. However, their

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #expd

C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-376/Product: prolactin receptor, short form Sia #status predicted <NAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 376;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
||| |||
DB 81 GGPNSCHFG 89

RESULT 47
A40144
5-aminomidazole ribonucleotide carboxylase-5-aminomidazole-4-N-succinocarboxamide ribo
C:Species: Gallus gallus (chicken)
C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 21-Jul-2000
C:Accession: A35641
R:Chen, Z.; Dixon, J.E.; Zalkin, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3097-3101, 1990
A:Title: Cloning of a chicken liver cDNA encoding 5-aminomidazole ribonucleotide carbox
ylase from a chicken liver mutant.
A:Reference number: A35641; MUID:90222176; PMID:1691501
A:Status: Preliminary
A:Cross-references: A35641
A:Molecule type: mRNA
A:Residues: 1-426 <CRS>
A:Cross-references: GDB:131764; NID:9211193; PIDN:AAA48601.1; PID:9211194
C:Superfamily: phosphoribosylaminimidazole carboxylase catalytic chain homology
F:267-398/Domain: phosphoribosylaminimidazole carboxylase catalytic chain homology <PC

Query Match 34.1%; Score 42; DB 2; Length 426;
Best Local Similarity 46.2%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWCK 16
||| |||
DB 90 AHCEWPIEWVCR 102

RESULT 48
E87375
conserved hypothetical protein CC1017 (imported); Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: E87375
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.G.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; EricTeava, M.; White, O.; Salzberg, S.L.; Shapiro, J.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4138-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: E87375
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-554 <STO>
A:Cross-references: GDB:A8005673; NID:913422303; PIDN:NAK23001.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC10:7

Query Match 34.1%; Score 42; DB 2; Length 554;
Best Local Similarity 35.0%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWCKPQGS 20
||| |||
DB 478 GGITASRFQALFWLSRONGG 497

RESULT 49
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C:Accession: A40144; A57018
R:Boutin, J.M.; Ederly, M.; Shiota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.
Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human
Mol. Endocrinol. 3, 1455-1461, 1989
A:Reference number: A40144; MUID:90114212; PMID:2558309
A:Accession: A40144
A:Molecule type: mRNA
A:Residues: 1-622 <BOU>
A:Cross-references: GDB:M31661; NID:g:90361; PIDN:AAA60174.1; PID:g190362
R:Fuhr, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
lines.
A:Reference number: A57018; MUID:95286597; PMID:7768908
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-references: GDB:S78505; NID:g999114; PIDN:AAB344470.1; PID:g999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <NAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.1%; Score 42; DB 2; Length 622;
Best Local Similarity 77.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTASCHFG 9
||| |||
DB 81 GGPNSCHFG 89

RESULT 50
T00636
hypothetical protein F21856.2 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 05-Nov-1999
C:Accession: T00636
R:Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.
rgescu, A.; Ayala, J.; Liu, S.; Bruce, R.; Quan, G.; Montgomery, M.; Ow, D.; Nolan, J.
submitted to the EMBL Data Library, January 1998
A:Description: Sequence analysis of a 3.5 Mb contig in 19p13.3 between CDC34 and D195
A:Reference number: 214195
A:Accession: T00636
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-679 <LAM>
A:Cross-references: EMBL:AC004030; NID:g2804590; PIDN:AAB97620.1; PID:g2804592
C:Genetics:
A:Map position: 19p13.3
A:Introns: 594/1; 637/3; 650/3
A>Note: F21856.2

Query Match 34.1%; Score 42; DB 2; Length 679;
Best Local Similarity 36.8%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 2 GTASCHFGELTWVCKPQGG 20
| | | | | : |
Db 98 GARDAHQGRPTWALRPDG 116

Search completed: November 5, 2003, 19:07:19
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:00:18 : Search time 11 Seconds
(without alignments)
85.503 Million cell updates/sec

Title: US-09-863-600E-19

Perfect score: 123

Sequence: 1 GGTASCHFGPLTWCKPQG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	58	47.2	19	LANC_STRSQ
2	55	44.7	19	DURC_STRGP
3	54	43.9	19	DURB_STRGW
4	50	40.7	19	DURA_STRGV
5	50	40.7	19	CINA_STRGV
6	47.5	38.6	731	HUTU_CAEEL
7	45.5	37.0	498	HELI_HSVI1
8	45	36.6	126	YMM2_YEAST
9	45	36.6	215	ERD2_ENTHI
10	45	36.6	346	YAMY_BACAD
11	44.5	36.2	337	CSL2_HUMAN
12	44	35.8	387	YB96_YEAST
13	44	35.8	421	P2X5_HUMAN
14	44	35.8	522	GA65_HUMAN
15	44	35.8	628	ABFA_ASPNG
16	44	35.8	735	AD02_MACFA
17	43.5	35.4	437	VIPS_RAT
18	43	35.0	123	MSS4_HUMAN
19	43	35.0	123	MSS4_MOUSE
20	43	35.0	123	MSS4_RAT
21	43	35.0	199	PDX1_HUMAN
22	43	35.0	397	YWO4_CAEEL
23	43	35.0	507	CRNA_EMEN1
24	43	35.0	676	HUTU_HUMAN
25	43	35.0	676	HUTU_MOUSE
26	42.5	34.6	96	Y189_ARCFU
27	42.5	34.6	347	IF32_YEAST
28	42.5	34.6	478	SEP4_HUMAN
29	42	34.1	199	PDX1_MOUSE
30	42	34.1	199	PDX1_RAT
31	42	34.1	426	PUR6_CHICK
32	42	34.1	502	PIV2_ADECR
33	42	34.1	622	PLRL_HUMAN

34	41.5	33.7	155	Y115_METJA
35	41.5	33.7	342	YPIX_CLOPE
36	41.5	33.7	892	HIC1_MOUSE
37	41.5	33.7	982	POL_HTLV2
38	41.5	33.7	1133	VGLM_HANTB
39	41.5	33.7	1133	VGLM_SEOUB
40	41.5	33.7	1133	VGLM_SEOUS
41	41.5	33.7	1134	VGLM_SEOUR
42	41	33.3	229	UNG_CHLMU
43	41	33.3	229	UNG_CHLTR
44	41	33.3	239	RNC_NEIMA
45	41	33.3	239	RNC_NEIMB
46	41	33.3	248	NADE_MYCGE
47	41	33.3	296	CYCG_RHOSH
48	41	33.3	330	TLX1_HUMAN
49	41	33.3	471	ORVB_ORYSA
50	41	33.3	814	AD15_HUMAN
51	41	33.3	815	AD15_MOUSE
52	41	33.3	873	LDVR_MOUSE
53	41	33.3	873	LDVR_RAT
54	41	33.3	906	RD14_ARATH
55	40.5	32.9	300	ERF5_ARATH
56	40.5	32.9	437	VIPS_MOUSE
57	40.5	32.9	566	HEMA_IADU3
58	40.5	32.9	1142	VGLM_PHV
59	40	32.5	71	CBA_CARPI
60	40	32.5	212	SSPA_HAEIN
61	40	32.5	343	LUM_CHICK
62	40	32.5	343	LUM_CONJA
63	40	32.5	359	LPFD_SALTY
64	40	32.5	425	PUR6_HUMAN
65	40	32.5	425	PUR6_MOUSE
66	40	32.5	425	PUR6_RAT
67	40	32.5	443	PHOR_PSEAE
68	40	32.5	468	TM11_HUMAN
69	40	32.5	511	AROF_LYCES
70	40	32.5	511	AROG_SOLTU
71	40	32.5	525	AROF_ARATH
72	40	32.5	529	C792_ARATH
73	40	32.5	549	FAST_HUMAN
74	40	32.5	694	UL31_HQWVA
75	40	32.5	790	AD30_HUMAN
76	40	32.5	963	TRES_THETH
77	40	32.5	1531	MRP1_HUMAN
78	39.5	32.1	153	SODC_HORSE
79	39.5	32.1	258	VSPI_TRIST
80	39.5	32.1	379	ADHX_ARATH
81	39.5	32.1	500	DPS1_YEAST
82	39.5	32.1	548	IDD_MOUSE
83	39.5	32.1	550	HEMA_IADHK
84	39.5	32.1	550	HEMA_IADH3
85	39.5	32.1	896	POL_HTLIA
86	39	31.7	126	RNS6_PIG
87	39	31.7	143	DSS4_YEAST
88	39	31.7	144	NOGG_RAT
89	39	31.7	192	MOBA_NEIMA
90	39	31.7	192	MOBA_NEIMB
91	39	31.7	195	VPRT_BLVU
92	39	31.7	232	NOGG_HUMAN
93	39	31.7	232	NOGG_MOUSE
94	39	31.7	265	MURI_BACSH
95	39	31.7	282	FU34_YEAST
96	39	31.7	308	Y964_SYNY3
97	39	31.7	345	CC14_CAEEL
98	39	31.7	350	ADH_SCHPO
99	39	31.7	359	ID12_METJA
100	39	31.7	410	PHT4_PSEPU

ALIGNMENTS

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LANC_STRSQ          STANDARD;          PRT;          19 AA.
AC F38655;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic anconevin.
OS Streptomyces sp. (strain A647P-2)
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
RP SEQUENCE.
RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Motoki Y.;
RT "The structure of anconevin, a new peptide inhibitor of angiotensin I
RT converting enzyme."
RT Tetrahedron Lett. 26:665-668(1985).
CC -!- FUNCTION: ACTS AS INHIBITOR OF ANGIOTENSIN I CONVERTING ENZYME.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
DR PIR; A61284; EWSMAN.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
FT SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;
Query Match 47.2%; Score 58; DB 1; Length 19;
Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 2; Indels C; Gaps 0;

QY 5 SCHFGPLTWC 15
DB 4 SCSYGLTWC 14

RESULT 2
DUPC_STRSQ          STANDARD;          PRT;          19 AA.
AC F36503;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic duramycin C.
OS Streptomyces griseolutes.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
CX NCBI_TaxID=29306;
RN [1]
RP SEQUENCE.
RC STRAIN=R2107;
RX MEDLINE=91107436; PubMed=2125590;
RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycins B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin."
RT J. Antibiot. 43:1403-1412(1990).
RN [2]
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RX MEDLINE=91107436; PubMed=2125590;
RA Raschdorf F., Peter H.H.;
RT "Solution structure of the lantibiotics duramycin B and C."
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C."
RL Eur. J. Biochem. 216:419-428(1993).
CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
FT SEQUENCE 19 AA; 2063 MW; 0133445E27362F00 CRC64;
Query Match 43.9%; Score 54; DB 1; Length 19;

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```

RT "Solution structures of the lantibiotics duramycin B and C.";
RL Eur. J. Biochem. 216:419-428(1993).
CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
FT SEQUENCE 19 AA; 2007 MW; E24045CE3F95286A CRC64;
Query Match 44.7%; Score 55; DB 1; Length 19;
Best Local Similarity 72.7%; Pred. No. 0.029;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SCHFGPLTWC 15
DB 4 SCSYGLTWC 14

RESULT 3
DUPC_STRSQ          STANDARD;          PRT;          19 AA.
AC F36502;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Lantibiotic duramycin B.
OS Streptococcus sp. (strain R2075).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=35759;
RN [1]
RP SEQUENCE.
RX MEDLINE=91107436; PubMed=2125590;
RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,
RA Raschdorf F., Peter H.H.;
RT "Duramycins B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinnamycin."
RT J. Antibiot. 43:1403-1412(1990).
RN [2]
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RX MEDLINE=91107436; PubMed=2125590;
RA Raschdorf F., Peter H.H.;
RT "Solution structure of the lantibiotics duramycin B and C."
RL (In) Schneider C.H., Eberles A.N. (eds.);
RL Peptides 1992, pp.519-520, Escom Science Publishers, Leiden (1993).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Fredenhagen A., Jung G.;
RT "Solution structure of the lantibiotics duramycin B and C."
RL Eur. J. Biochem. 216:419-428(1993).
CC -!- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.
CC -!- PTM: Maturation of lantibiotics involves the enzymic conversion of
CC Thr, and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLNK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 4 14 Lanthionine (Ser-Cys).
FT CROSSLNK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLNK 6 19 Lysinoalanine (Ser-Lys).
FT SEQUENCE 19 AA; 2063 MW; 0133445E27362F00 CRC64;
Query Match 43.9%; Score 54; DB 1; Length 19;

```

RESULT 5	CINA_STRGV	STANDARD;	PRT;	78 AA.
ID	CINA_STRGV			
AC	P29827;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-APR-1993 (Rel. 25, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Lanthibiotic cinnamycin precursor (Lanthiopeptin) (Lanthibiotic RO 09-0198).			
DE				
GN	CINA OR ROCA.			
OS	Streptovorticillum griseovorticillatum.			
OS	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycineae; Streptomycetaceae; Streptomycetes.			
OC				

```

RESULT 6
HUTU CAEEL
ID HUTU CAEEL STANDARD; PRT: 731 AA.
AC Q9NAE2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable urocanate hydratase (EC 4.2.1.49) (Urocanase)

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```
DE (Imidazole)propionate hydrolase).
GN Y51H4A.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_taxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Sulston J.E.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3H-imidazol-4-
CC y1)propanoate = urocanate + H(2)O.
CC -!- COFACTOR: NA2 (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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CC
DR EMBL; AL132952; CAB61139.1; -.
DR WormPep; Y51H4A.7; CE22333.
DR InterPro; IPR000193; Urocanase.
DR Pfam; PF011175; Urocanase; 1.
DR ProDom; PD025423; Urocanase; 1.
DR PROSITE; PS01233; UROCANASE; 1.
KW Hypothetical protein; Histidine metabolism; lyase; NA2.
SQ SEQUENCE 731 AA; 81523 MW; 891E1F61C9A604E6 CRC64;
Query Match 38.6%; Score 47.5; DB 1; Length 731;
Best Local Similarity 47.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 7; Indels 3; Gaps 1;
QY 1 GGTASCHFGPLTWVC---KQ 18
DB 496 GDFSMGFGPRWCTSGKPE 516
RESULT 7
HSL1_HSV11
ID HSL1_HSV11 STANDARD; PRT; 498 AA.
AC Q00092;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Probable helicase.
GN 25.
OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Ictalurid Herpes-like viruses.
OX NCBI_taxID=10403;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Auburn 1;
RC MEDLINE=92087490; PubMed=1727613;
RA Davison A.J.;
RT "Channel catfish virus; a new type of herpesvirus.";
RL Virology 186:9-14(1992).
CC
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CC
EMBL; M75136; AAA88128.1; -.
28
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DR PIR; H36788; HJBE11
KW Helicase; ATP-binding.
FT NP_BIND 37 44 ATP (POTENTIAL).
SQ SEQUENCE 498 AA; 55761 MW; 445F6185FE121AEF CRC64;
Query Match 37.0%; Score 45.5; DB 1; Length 498;
Best Local Similarity 56.2%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;
QY 1 GGTASCHFGPLTWVC 15
DB 323 GGSASCRFGALIEYMC 338
[[::]]] ||| ::|
RESULT 8
YMM2_YEAST STANDARD; PRT; 126 AA.
ID YMM2_YEAST
AC Q03207;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypothetical 14.5 kDa protein in PHO84-GTR1 intergenic region.
GN YML122C OR YW7056.04C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_taxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII."
RL Nature 387:90-93(1997).
CC
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CC
EMBL; Z49218; CAA89158.1; -.
DR PIR; S54062; S54062.
DR SGD; S0004591; YML122C.
KW Hypothetical protein.
SQ SEQUENCE 126 AA; 14472 MW; EF8049302E3D235A CRC64;
Query Match 36.6%; Score 45; DB 1; Length 126;
Best Local Similarity 53.8%; Pred. No. 5.4;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 TASCCHFGPLTWVC 15
DB 53 TARCQFNSTWTC 65
[[::]]] ||| |||
RESULT 9
ERD2_ENTH1 STANDARD; PRT; 215 AA.
ID ERD2_ENTH1
AC O44017;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ER lumen protein retaining receptor.
GN ERD2.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
```

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CC NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK-9;
RA Sanchez-Lopez R., Gama-Castro S., Ramos M.A., Merino E., Lizardi P.M.,
RA Alagon A.;
RT "Cloning and expression of the Entamoeba histolytica ERD2 gene.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC
CC -!- FUNCTION: Required for the retention of luminal endoplasmic
CC reticulum proteins. Determines the specificity of the luminal ER
CC protein retention system. Also required for normal vesicular
CC traffic through the Golgi (By similarity).
CC
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC
CC -!- SIMILARITY: BELONGS TO THE ERD2 FAMILY.
CC
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CC
CC EMBL; Z22520; CAAB0248.1; -
CC PIR; S34732; S34732.
CC DR Pfam; PF04171; DUF405; 1.
CC DR Pfam; PF04235; DUF418; 1.
CC KM Hypothetical protein; Transport; Transmembrane.
CC FT TRANSMEM 15 35 POTENTIAL.
CC FT TRANSMEM 55 75 POTENTIAL.
CC FT TRANSMEM 93 113 POTENTIAL.
CC FT TRANSMEM 139 159 POTENTIAL.
CC FT TRANSMEM 182 202 POTENTIAL.
CC FT TRANSMEM 229 249 POTENTIAL.
CC FT TRANSMEM 269 289 POTENTIAL.
CC FT TRANSMEM 295 315 POTENTIAL.
CC SQ SEQUENCE 346 AA; 39876 MW; A46DF6009FCF9B92 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 215;
Best Local Similarity 46.2%; Pred. No. 8.7;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Oy 3 TASCHFGPLTWVC 15
Db 174 TEQSYMSPLTWIC 186
| : : : : :
| : : : : :

RESULT 10
YAMY BACAD
ID YAMY BACAD STANDARD; PRT; 346 AA.
AC P32819;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 39.9 kDa protein in amylase 3' region.
OS Bacillus acidopulluliticus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=28030;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelly A.P., Diderichsen B., Jorgensen S.T., McConnell D.J.;
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN TRANSPORT (POTENTIAL).
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CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: STRONG, TO E-COLI YEIB, B-SUBTILIS YXAH (S14H) AND
CC B-SUBTILIS YRKO.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z22520; CAAB0248.1; -
CC PIR; S34732; S34732.
CC DR Pfam; PF04171; DUF405; 1.
CC DR Pfam; PF04235; DUF418; 1.
CC KM Hypothetical protein; Transport; Transmembrane.
CC FT TRANSMEM 15 35 POTENTIAL.
CC FT TRANSMEM 55 75 POTENTIAL.
CC FT TRANSMEM 93 113 POTENTIAL.
CC FT TRANSMEM 139 159 POTENTIAL.
CC FT TRANSMEM 182 202 POTENTIAL.
CC FT TRANSMEM 229 249 POTENTIAL.
CC FT TRANSMEM 269 289 POTENTIAL.
CC FT TRANSMEM 295 315 POTENTIAL.
CC SQ SEQUENCE 346 AA; 39876 MW; A46DF6009FCF9B92 CRC64;

Query Match 36.6%; Score 45; DB 1; Length 346;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 CHFGPLTWV 14
Db 319 CKFGPLEWV 327
| : : : :
| : : : :

RESULT 11
ID C5L2_HUMAN STANDARD; PRT; 337 AA.
AC Q9P296;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Csa anaphylatoxin chemotactic receptor C5L2.
GN GPR77 OR C5L2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ohno M., Hirata T., Enomoto M., Araki T., Sato K., Ishimaru H.,
RA Takahashi T.A.;
RT "A putative chemoattractant receptor, C5L2 is expressed in granulocyte
RT and immature dendritic cells, but mature dendritic cells.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21105913; PubMed=11165367;
RA Lee D.K., George S.R., Cheng R., Nguyen T., Liu Y., Brown M.,
RA Lynch K.R., O'Dowd B.F.;
RT "Identification of four novel human G protein-coupled receptors
RT expressed in the brain.";
RL Brain Res. Mol. Brain Res. 86:13-22(2001).
RN [3]
RP FUNCTION.
RX TISSUE=Brain;
RX MEDLINE=21850712; PubMed=11773063;
RA Cain S.A., Monk P.N.;
RT "The orphan receptor C5L2 has high affinity binding sites for
RT complement fragments C5a and C5a des Arg(74).";
RL J. Biol. Chem. 277:7165-7169(2002).
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CC -!- FUNCTION: Receptor for the chemotactic and inflammatory peptide
CC anaphylatoxin C5a, C4a and C3a and their des arginated
CC derivatives. Couples weakly to Gi-mediated signalling pathways.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Frontal cortex, hippocampus, hypothalamus,
CC pons and liver.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC -----
DR EMBL; AB038237; BAA95414.1; -
DR EMBL; AF317655; AAK12640.1; -
DR Genbank; HGNC:4527; GPR77.
DR GO; GO:0016526; F:G-protein coupled receptor, unknown ligand . . . ; NAS.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7-m.1; 1.
DR PRINTS; PR00237; GPCRHOODPSN
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; FALSE NEG.
DR PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 38 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 39 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 62 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 95 2 (POTENTIAL).
FT DOMAIN 96 114 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 115 137 3 (POTENTIAL).
FT DOMAIN 138 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 172 4 (POTENTIAL).
FT DOMAIN 173 202 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 225 5 (POTENTIAL).
FT DOMAIN 226 237 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 294 7 (POTENTIAL).
FT DOMAIN 295 337 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT DISULFID 107 186 BY SIMILARITY.
SQ SEQUENCE 337 AA; 36080 MW; 53AF41B129FE8FE6 CRC64;

Query Match 36.2%; Score 44.5; DB 1; Length 337;
Best Local Similarity 47.4%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 6; Indels 3; Gaps 1;

QY 4 ASCHFGPLTWV--CKPGS 19
||| | | | | | | | |
DB 217 ASCHSALLCWARRCRPLG 235

RESULT 12
YB96 YEAST
ID YB96 YEAST STANDARD; PRT: 387 AA.
AC P38332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 43.3 kDa protein in ALG7-EN7; intergenic region.
GN YBR246W OR YBR1634
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Aljinovic G., Pohl F.M., Pohl T.M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -----

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CC -----
DR EMBL; Z36115; CAA85209.1; -
DR PIR; S46123; S46123.
DR SGD; S0000450; YBR246W.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
KW Hypothetical protein.
SQ SEQUENCE 387 AA; 43308 MW; 97CAFD285BC11456 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 387;
Best Local Similarity 69.2%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 4 ASCHFGPLTWVCK 16
||| | | | | | | |
DB 125 ASCHFSLD--CK 135

RESULT 13
P2X5 HUMAN
ID P2X5 HUMAN STANDARD; PRT: 421 AA.
AC Q93086; O43450; Q75540; Q93087; Q9NZV0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2X purinoceptor 5 (ATP receptor) (P2X5) (Purinegic receptor).
DE P2X5 OR P2X5.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RA Tokuyama Y., Meru L., Chen X., Rouard M., Bell G.I.;
RT "Cloning of human P2X purinoceptor new subtype (P2X5).";
RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A).
RC TISSUE=Brain;
RX MEDLINE=98074936; PubMed=9414125;
RA Le K.-T., Paquet M., Nouel D., Babinski K., Seguela P.;
RT "Primary structure and expression of a naturally truncated human P2X
RT ATP receptor subunit from brain and immune system.";
RL FEBS Lett. 418:195-199(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM B).
RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RX MEDLINE=20138496; PubMed=10673275;
RA Touchman J.W., Aniketer Y., Dietrich N.L., Maduro V.V., McDowell G.,
RA Shetlersuk V., Bouffard G.G., Beckstrom-Sternberg S.M., Gahl W.A.,
RA Green E.D.;
RT "The genomic region encompassing the nephropathic cystinosis gene
RT (CTNS): complete sequencing of a 200-kb segment and discovery of a
RT novel gene within the common cystinosis-causing deletion.";
RL Genome Res. 10:165-173(2000).
CC -!- FUNCTION: RECEPTOR FOR ATP THAT ACTS AS A LIGAND GATED ION
CC CHANNEL.
CC -!- SUBUNIT: HOMO- OR HETEROPOLYMERS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;

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CC Isoid=Q93086-1; Sequence=Displayed;
CC Names=;
CC Isoid=Q93086-2; Sequence=VSP_004503;
CC !- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND IMMUNE
CC SYSTEM.
CC !- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
CC -----
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CC -----
DR EXBL; U49395; AAB08576.1; -
DR EMBL; U49396; AAB08577.1; -
DR EMBL; AF016709; AAC51931.1; -
DR EMBL; AF070573; AAC28645.1; -
DR EMBL; AF168787; AAF43106.1; ALT_SEQ.
DR EMBL; AF168787; AAF43105.1; -
DR Genew; HGNC:8536; P2RX5.
DR MIM; 602836; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005216; F: ion channel activity; TAS.
DR GO; GO:0004899; F: transmembrane receptor activity; TAS.
DR GO; GO:0007399; P: neurogenesis; TAS.
DR GO; GO:0007165; P: signal transduction; TAS.
DR GO; GO:0006832; P: small molecule transport; TAS.
DR InterPro; IPR001429; P2X receptor.
DR Pfam; PF00864; P2X receptor; 1.
DR PRINTS; PR01307; P2XRECEPTOR.
DR TIGRFAMs; TIGR00863; P2X; 1.
DR PROSITE; PS01212; P2X RECEPTOR; 1.
DR Ionic channel; Transmembrane; Ion transport; Receptor; Glycoprotein;
KW Alternative splicing.
FT DOMAIN 1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 1 (POTENTIAL).
FT DOMAIN 52 318 EXTRACELLULAR, CYSTEINE-RICH (POTENTIAL).
FT TRANSMEM 319 339 2 (POTENTIAL).
FT DOMAIN 340 421 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 97 98 Missing (in isoform B).
FT CONFLICT 156 156 /FTID=VSP_004503.
FT CONFLICT 204 204 GE -> EK (IN REF. 1).
FT CONFLICT 236 237 E -> G (IN REF. 2).
FT CONFLICT 250 250 S -> SK (IN REF. 2).
FT CONFLICT 329 329 VI -> IV (IN REF. 2).
FT CONFLICT 351 351 E -> R (IN REF. 2).
FT CONFLICT 351 351 P -> S (IN REF. 1).
FT CONFLICT 398 399 E -> Q (IN REF. 1).
FT CONFLICT 399 399 KR -> NV (IN REF. 1).
SQ SEQUENCE 421 AA; 47103 MW; 6B47307AA14C2A6C CRC64;
Query Match 35.8%; Score 44; DB 1; Length 421;
Best Local Similarity 63.6%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 SCHFGPLTWVC 15
DB 218 SCHFGPKNHYC 228
RESULT 14
ID GAB5_HUMAN STANDARD; PRT; 522 AA.
AC P34059;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE N-acetylgalactosamine-6-sulfatase precursor (EC 3.1.6.4) (N-
acetylgalactosamine-6-sulfate sulfatase) (Galactose-6-sulfate
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DE sulfatase) (GalNAc6S sulfatase) (Chondroitinsulfatase)
DR (Chondroitinase).
GN GALNS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=92095973; PubMed=1755850;
RA Tomatsu S., Fukuda S., Masue M., Sukegawa K., Fukao T., Yamagishi A.,
RA Hori T., Iwata H., Ogawa T., Nakashima Y., Hanyu Y., Hashimoto T.,
RA Titani K., Oyama R., Suzuki M., Yagi K., Hayashi Y., Orii T.;
RA "Morquio disease: isolation, characterization and expression of full-
RT length cDNA for human N-acetylgalactosamine-6-sulfate sulfatase.";
RL Biochem. Biophys. Res. Commun. 181:677-683(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95095267; PubMed=8001980;
RA Morris C.P., Guo X.H., Apostolou S., Hopwood J.J., Scott H.S.;
RA "Morquio A syndrome: cloning, sequence, and structure of the human N-
RT acetylgalactosamine 6-sulfatase (GALNS) gene.";
RL Genomics 22:652-654(1994).
RN [3]
RP VARIANT MPS-IVA LYS-204.
RX MEDLINE=92395122; PubMed=152213;
RA Fukuda S., Tomatsu S., Masue M., Sukegawa K., Iwata H., Ogawa T.,
RA Nakashima Y., Hori T., Yamagishi A., Hanyu Y., Morooka K., Kiman T.,
RA Hashimoto T., Orii T.;
RA "Mucopolysaccharidosis type IVA. N-acetylgalactosamine-6-sulfate
RT sulfatase exonic point mutations in classical Morquio and mild
RT cases.";
RL J. Clin. Invest. 90:1049-1053(1992).
RN [4]
RP VARIANTS MPS-IVA.
RX MEDLINE=95397840; PubMed=7668283;
RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Maruf Rezvi G.,
RA Yamagishi A., Yamada N., Kato Z., Isogai K., Sukegawa K., Kondo N.,
RA Suzuki Y., Shinozawa N., Orii T.;
RA "Mucopolysaccharidosis IVA: identification of a common missense
RT mutation I113F in the N-Acetylgalactosamine-6-sulfate sulfatase
RT gene.";
RL Am. J. Hum. Genet. 57:556-563(1995).
RN [5]
RP VARIANTS MPS-IVA.
RX MEDLINE=95315929; PubMed=7795586;
RA Ogawa T., Tomatsu S., Fukuda S., Wraith J.E., Maruf Rezvi G.,
RA Sukegawa K., Kondo N., Suzuki Y., Shinozawa N., Orii T.;
RA "Mucopolysaccharidosis IVA: screening and identification of mutations
RT of the N-acetylgalactosamine-6-sulfate sulfatase gene.";
RL Hum. Mol. Genet. 4:341-349(1995).
RN [6]
RP VARIANTS MPS-IVA ARG-77; TRP-90; VAL-96; LEU-151; GLY-230 AND THR-291.
RX MEDLINE=95359983; PubMed=7633425;
RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Maruf Rezvi G.,
RA Yamagishi A., Yamada N., Kato Z., Isogai K., Sukegawa K., Kondo N.,
RA Suzuki Y., Shinozawa N., Orii T.;
RA "Mucopolysaccharidosis type IVA: identification of six novel
RT mutations among non-Japanese patients.";
RL Hum. Mol. Genet. 4:741-743(1995).
RN [7]
RP VARIANT MPS-IVA SER-487.
RX MEDLINE=96047158; PubMed=7581409;
RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Yamada N., Isogai K.,
RA Kato Z., Sukegawa K., Kondo N., Suzuki Y., Shinozawa N., Orii T.;
RA "Two new mutations, Q473X and N487S, in a Caucasian patient with
RT mucopolysaccharidosis IVA (Morquio disease).";
RL Hum. Mutat. 6:195-196(1995).
RN [8]
RP VARIANTS MPS-IVA ALA-138; SER-151 AND LEU-151.
RX MEDLINE=96216146; PubMed=8651279;
RA Tomatsu S., Fukuda S., Yamagishi A., Cooper A., Wraith J.E., Hori T.,
```

RA Kato Z., Yamada N., Isogai K., Sukegawa K., Kondo N., Suzuki Y., Shimozawa N., Orii T.;
 RA "Mucopolysaccharidosis IVA: four new exonic mutations in patients with N-acetylgalactosamine-6-sulfate sulfatase deficiency."; Am. J. Hum. Genet. 58:950-962(1996). [9]
 RN
 RP VARIANTS MPS-IVA CYS-94 AND VAL-97. MEDLINE=96423834; PubMed=9826435;
 RX
 RA Cole D.E.C., Fukuda S., Gordon B.A., Rip J.W., Lecouteur A.N., Rupa C.A., Tomatsu S., Ogawa T., Sukegawa K., Orii T.;
 RA "Heteroallelic missense mutations of the galactosamine-6-sulfate sulfatase (GALNS) gene in a mild form of Morquio disease (MPS IVA)."; Am. J. Med. Genet. 63:558-565(1996). [10]
 RN
 RP VARIANTS MPS-IVA. MEDLINE=97442274; PubMed=9298823;
 RX
 RA Bunge S., Kleijer W.J., Tytki-Szymanska A., Steglich C., Beck M., Tomatsu S., Fukuda S., Poorthuis B.J.H.M., Czartoryska B., Orii T., Gal A.;
 RA "Identification of 31 novel mutations in the N-acetylgalactosamine-6-sulfatase gene reveals excessive allelic heterogeneity among patients with Morquio A syndrome."; Hum. Mutat. 10:223-232(1997). [11]
 RN
 RP VARIANTS MPS-IVA. MEDLINE=98041700; PubMed=9375852;
 RX
 RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Ferreira P., di Natale P., Tortora P., Fujimoto A., Kato Z., Yamada N., Isogai K., Yamagishi A., Sukegawa K., Suzuki Y., Shimozawa N., Kondo N., Sij W.S., Orii T.;
 RA "Fourteen novel mucopolysaccharidosis IVA producing mutations in GALNS gene."; Hum. Mutat. 10:368-375(1997). [12]
 RN
 RP VARIANTS MPS-IVA. MEDLINE=98180718; PubMed=9521421;
 RX
 RA Yamada N., Fukuda S., Tomatsu S., Muller V., Hopwood J.J., Nelson J., Kato Z., Yamagishi A., Sukegawa K., Kondo N., Orii T.;
 RA "Molecular heterogeneity in mucopolysaccharidosis IVA in Australia and Northern Ireland: nine novel mutations including T312S, a common allele that confers a mild phenotype."; Hum. Mutat. 11:202-208(1998). [13]
 RN
 RP VARIANTS SER-393 AND MET-488. MEDLINE=98112415; PubMed=9452036;
 RX
 RA Tomatsu S., Fukuda S., Cooper A., Wraith J.E., Yamagishi A., Kato Z., Yamada N., Isogai K., Sukegawa K., Suzuki Y., Shimozawa N., Kondo N., Orii T.;
 RA "Fifteen polymorphisms in the N-acetylgalactosamine-6-sulfate sulfatase (GALNS) gene: diagnostic implications in Morquio disease."; Hum. Mutat. Suppl. 1:S42-S46(1998). [14]
 CC
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 6-sulfate groups of the N-acetyl-D-galactosamine 6-sulfate units of chondroitin sulfate and of the D-galactose 6-sulfate units of keratan sulfate.
 CC
 CC -!- SUBUNIT: OLIGOMER OF DISULFIDE LINKED 40- AND 15-KDA POLYPEPTIDES. [15]
 CC
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC
 CC -!- DISEASE: Defects in GALNS are the cause of mucopolysaccharidosis type IVA (MPS-IVA) [MIM:253000]; also known as Morquio A syndrome. MPS-IVA is characterized by specific spondyloepiphyseal dysplasia, short trunk dwarfism, coxa vara, odontoid hypoplasia, corneal opacities, preservation of intelligence, and excessive urinary excretion of keratan sulfate and chondroitin-6-sulfate. Severely affected patients usually die of cardiopulmonary disturbance or cervical cord compression in the second or third decade of life.
 CC
 CC -!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
 CC
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CC EMBL; D17629; BAA04535.1;
 DR EMBL; D17616; BAA04535.1; JOINED.
 DR EMBL; D17617; BAA04535.1; JOINED.
 DR EMBL; D17618; BAA04535.1; JOINED.
 DR EMBL; D17619; BAA04535.1; JOINED.
 DR EMBL; D17620; BAA04535.1; JOINED.
 DR EMBL; D17621; BAA04535.1; JOINED.
 DR EMBL; D17622; BAA04535.1; JOINED.
 DR EMBL; D17623; BAA04535.1; JOINED.
 DR EMBL; D17624; BAA04535.1; JOINED.
 DR EMBL; D17625; BAA04535.1; JOINED.
 DR EMBL; D17626; BAA04535.1; JOINED.
 DR EMBL; D17628; BAA04535.1; JOINED.
 DR EMBL; U06088; AAC51350.1;
 DR EMBL; U06078; AAC51350.1; JOINED.
 DR EMBL; U06079; AAC51350.1; JOINED.
 DR EMBL; U06080; AAC51350.1; JOINED.
 DR EMBL; U06081; AAC51350.1; JOINED.
 DR EMBL; U06082; AAC51350.1; JOINED.
 DR EMBL; U06083; AAC51350.1; JOINED.
 DR EMBL; U06084; AAC51350.1; JOINED.
 DR EMBL; U06085; AAC51350.1; JOINED.
 DR EMBL; U06086; AAC51350.1; JOINED.
 DR EMBL; U06087; AAC51350.1; JOINED.
 DR PIR; JQ1299; KJHUG6.
 DR HSSP; P15848; IFSU.
 DR Genew; HGNC:4122; GALNS.
 DR MIM; 253000;
 DR GO; GO:0003943; F:N-acetylgalactosamine-4-sulfatase activity; TAS.
 DR InterPro; IPR000917; Sulfatase.
 DR Pfam; PF00884; Sulfatase; 1.
 DR PROSITE; PS00523; SULFATASE_1; 1.
 DR PROSITE; PS00149; SULFATASE_2; 1.
 KW Hydrolase; Glycoprotein; Signal; Lysosome; Mucopolysaccharidosis; Disease mutation; Polymorphism; Dwarfism.
 FT SIGNAL 1 26
 FT CHAIN 27 522 N-ACETYL GALACTOSAMINE-6-SULFATASE.
 FT MOD_RES 79 79 2-AMINO-3-OXOPROPIONIC ACID (BY SIMILARITY).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 47 47 G -> R (IN MPS-IVA; SEVERE FORM).
 FT VARIANT 60 60 /FTID=VAR_007172
 FT VARIANT 67 67 D -> N (IN MPS-IVA; MILD FORM).
 FT VARIANT 67 67 /FTID=VAR_007173
 FT VARIANT 67 67 L -> M (IN MPS-IVA; ASSOCIATED WITH S-409
 Query Match 35.8%; Score 44; DB 1; Length 522;
 Best Local Similarity 43.8%; Pred. No. 28;
 Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 2 GTASCHFGPLTWCKP 17
 Db 161 GSPNCHFGFYDNKARP 176
 RESULT 15
 ID ABFA ASPNG STANDARD; PRT; 628 AA.
 AC P42254;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Alpha-L-arabinofuranosidase A precursor (EC 3.2.1.55) (Arabinosidase A) (ABP A).
 GN ABFA.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=5061;
 RN [1]_TaxID=5061;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 26-35 AND 63-77.

```

RC STRAIN=CBS 120.49 / N400;
RX MEDLINE=95093616; PubMed=8000538;
RA Flippini M.J.A., Visser J., van der Veen P., de Graaff L.H.;
RT "Arabinase gene expression in Aspergillus niger: indications for
RL coordinated regulation.";
RL Macrobiology 140:2673-2682(1994).
CC -!- FUNCTION: ACTS ONLY ON SMALL LINEAR 1,5-ALPHA-LINKED
CC L-ARABINOFURANOSYL OLIGOSACCHARIDES.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal non-reducing alpha-L-
CC arabinofuranoside residues in alpha-L-arabinosides.
CC -!- PATHWAY: Plant cell wall polysaccharide L-arabinan degradation.
CC -!- SIMILARITY: BELONGS TO FAMILY 51 OF GLYCOSYL HYDROLASES.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29005; AAC41644.1; --
DR EMBL; A27979; CAA01904.1; --
KW Hydrolase; Glycosidase; Glycoprotein; Signal.
FT SIGNAL 1 25
FT CHAIN 26 628 ALPHA-L-ARABINOFURANOSIDASE A.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 493 493 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 628 AA; 67832 MW; 4F3E478F93468AD CRC64;

Query Match 35.8%; Score 44; DB 1; Length 628;
Best Local Similarity 47.1%; Pred. No. 33;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQG 19
Dd 535 TSUSDGFLYWASSAG 551

RESULT 16
AD02 MACFA
AC Q28478; 028472; STANDARD; PRT; 735 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
DE (Fertilin beta subunit) (PH-30) (PH30) (PH30-beta).
GN ADAM2 OR FTNB.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI TaxID=9541;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95260313; PubMed=7741716;
RA Perry A.C.F., Gichuhi P.M., Jones R., Hall L.;
RT "Cloning and analysis of monkey fertilin reveals novel alpha subunit
RT isoforms.";
RL Biochem. J. 307:843-850(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96341733; PubMed=8720115;

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RA Ramarao C.S., Myles D.G., White J.M., Primakoff P.;
RT "Initial evaluation of fertilin as an immunocontraceptive antigen and
RT molecular cloning of the cynomolgus monkey fertilin beta subunit.";
RL Mol. Reprod. Dev. 43:70-75(1996).
CC -!- FUNCTION: Sperm surface membrane protein that may be involved in
CC sperm-egg plasma membrane adhesion and fusion during
CC fertilization. Could have a direct role in sperm-zona binding or
CC migration of sperm from the uterus into the oviduct. Interactions
CC with egg membrane could be mediated via binding between its
CC disintegrin-like domain to one or more integrins receptors on the
CC egg. This is a non catalytic metalloprotease-like protein (By
CC similarity).
CC -!- SUBUNIT: Heterodimer with ADAM1/fertilin alpha.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed specifically in testis.
CC -!- DOMAIN: A tripeptide motif (PDE) within disintegrin-like domain
CC could be involved in the binding to egg integrin receptor and thus
CC could mediate sperm/egg binding (By similarity).
CC -!- PTM: The signal and the metalloprotease domain are cleaved during
CC the epididymal maturation of the spermatozoa (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X77653; CAA54733.1; --
DR EMBL; U33959; AAB52699.1; --
DR PIR; G02937; G02937.
DR HSP; P17494; 1KST.
DR MEROPS; M12_950; --
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Repolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; 1.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE NEG.
DR PROSITE; PS01186; EGF_2; FALSE NEG.
KW Cell adhesion; Signal; transmembrane; EGF-like domain; Glycoprotein.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 174 BY SIMILARITY.
FT CHAIN 175 735 ADAM 2.
FT DOMAIN 17 686 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 687 707 POTENTIAL.
FT DOMAIN 708 735 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 175 382 METALLOPROTEASE-LIKE.
FT DOMAIN 383 475 DISINTEGRIN-LIKE.
FT DOMAIN 476 606 CYS-RICH.
FT DOMAIN 612 645 EGF-LIKE.
FT DISULFID 287 370 BY SIMILARITY.
FT DISULFID 329 354 BY SIMILARITY.
FT DISULFID 445 458 POTENTIAL.
FT DISULFID 616 627 BY SIMILARITY.
FT DISULFID 621 633 BY SIMILARITY.
FT DISULFID 635 644 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 459 459 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 566 566 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 723 723 S -> T (IN REF. 2).
SQ SEQUENCE 735 AA; 82357 MW; BE84BE115E:DCB53 CRC64;

Query Match 35.8%; Score 44; DB 1; Length 735;
Best Local Similarity 44.0%; Pred. No. 38;
Matches 11; Conservative 1; Mismatches 3; Indels 10; Gaps 2;

QY 1 GGTASC---HF-----GPLTWVC 15
   ||||| || |||||
DB 460 GTSASCPENHIQTGHPGPNQWVC 484

RESULT 17
VIPS_RAT
ID VIPS_RAT STANDARD; PRT; 437 AA.
AC P35000;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Vasoactive intestinal polypeptide receptor, 2 precursor (VIP-R-2)
DE (Pituitary adenylate cyclase activating polypeptide type III receptor)
DE (PACAP type III receptor) (PACAP-R-3).
GN VIPR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
CX NCBI_TaxID=10116;
RN (1)
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=olfactory bulb;
RX MEDLINE=94039806; PubMed=8224221;
RA Lutz E.-M., Sheward W.J., West K.M., Morrow J.A., Fink G.,
  Harmar A.J.;
  "The VIP2 receptor: molecular characterization of a cDNA encoding a
  novel receptor for vasoactive intestinal peptide.";
  FEBS Lett. 334:3-8(1993).
RN (2)
SEQUENCE FROM N.A.
RC TISSUE=Brain Cortex;
RX MEDLINE=95580140; PubMed=7988457;
RA Usdin T.B., Bonner T.I., Mezey E.;
  "Two receptors for vasoactive intestinal polypeptide with similar
  specificity and complementary distributions.";
  RL Endocrinology 135:2662-2680(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27.
  THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
  CC -!- ACTIVATE ADENYLATE CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
  CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
  CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G PROTEIN COUPLED RECEPTORS.
  CC -----
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KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 437
FT RECEPTOR 2.
FT DOMAIN 23 125
   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 150
   1 (POTENTIAL).
FT DOMAIN 151 157
   CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 158 177
   2 (POTENTIAL).
FT DOMAIN 178 202
   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 203 226
   3 (POTENTIAL).
FT DOMAIN 227 239
   CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 261
   4 (POTENTIAL).
FT DOMAIN 262 278
   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 302
   5 (POTENTIAL).
FT DOMAIN 303 327
   CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 328 347
   6 (POTENTIAL).
FT DOMAIN 348 359
   EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 360 379
   7 (POTENTIAL).
FT DOMAIN 380 437
   CYTOPLASMIC (POTENTIAL).
FT DISULFID 201 270
   BY SIMILARITY.
FT CARBOHYD 57 57
   N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 87 87
   N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 91 91
   N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 383 383
   C -> R (IN REF. 2).
SQ SEQUENCE 437 AA; 49552 MW; 7E10218A9EE31360 CRC64;

Query Match 35.4%; Score 43.5; DB 1; Length 437;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 2 GTASCFGPLTWV-CK 16
   ||||| ||||| |||||
DB 187 GTLRCHDQPGSWGCK 202

RESULT 18
MSS4_HUMAN
ID MSS4_HUMAN STANDARD; PRT; 123 AA.
AC P47224; Q92992;
DT 01-FEB-1996 (Rel. 33, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 15-SEP-2003 (Rel. 42, Last annotation update);
DE Guanine nucleotide exchange factor MSS4 (Rab interacting factor).
GN RABIF OR RASGRF3 OR MSS4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN (1)
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95345082; PubMed=7619808;
RA Yu H., Schreiber S.L.;
  "Cloning, Zn2+ binding, and structural characterization of the
  RT guanine nucleotide exchange factor human MSS4.";
  RL Biochemistry 34:9103-9110(1995).
RN (2)
SEQUENCE FROM N.A.
RX MEDLINE=98110574; PubMed=9441742;
RA Mueller-Pillaech F., Zimmerhackl F., Lacher U., Schultz N.,
  RA Hameister H., Varga G., Friess H., Buechler M., Adler G., Gress T.M.;
  "Cloning of novel transcripts of the human guanine-nucleotide-exchange
  RT factor Mss4: in situ chromosomal mapping and expression in pancreatic
  RT cancer.";
  RL Genomics 46:389-396(1997).
RN (3)
SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
  RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
  RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP STRUCTURE BY NMR.
 RX MEDLINE=9537975; PubMed=7651540;
 RA Yu H., Schreiber S.L.;
 RT "Structure of guanine-nucleotide-exchange factor human Mss4 and
 RT identification of its Rab-interacting surface";
 RL Nature 376:788-791(1995).
 CC -!- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
 CC MEMBERS OF THE SEC4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
 CC FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
 CC THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
 CC TRANSPORT.
 CC -!- TISSUE SPECIFICITY: Ubiquitous
 CC -!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S78873; AAB34955.1; -;
 DR EMBL: U74324; AAB18264.1; -;
 DR EMBL: BC018488; AAB18488.1; -;
 DR PIR: I52427; I52427.
 DR PDB: IFWQ; 04-OCT-00.
 DR Genew: HGNC:9797; RAB1P.
 DR MIM: 603417; -;
 DR GO: GO:0005085; F:guanyl-nucleotide exchange factor activity; TAS.
 DR GO: GO:0006944; P:membrane fusion; TAS.
 DR GO: GO:0006899; P:non-selective vesicle transport; TAS.
 DR Pfam: PF044421; Mss4; 1.
 KW Guanine-nucleotide releasing factor; Protein transport; Zinc;
 KM 3D-structure.
 FT METAL 23 ZINC.
 FT METAL 26 ZINC.
 FT METAL 94 ZINC.
 FT METAL 97 ZINC.
 FT CONFLICT 5 6 EQ -> DE (IN REF. 1).
 FT STRAND 11 11
 FT STRAND 16 17
 FT STRAND 21 23
 FT TURN 24 27
 FT STRAND 28 31
 FT TURN 33 34
 FT STRAND 37 38
 FT STRAND 43 45
 FT TURN 48 49
 FT TURN 56 57
 FT STRAND 63 65
 FT STRAND 68 71
 FT HELIX 74 76
 FT STRAND 83 83
 FT STRAND 89 92
 FT TURN 95 96

FT STRAND 103 106
 FT TURN 110 111
 FT STRAND 113 116
 FT TURN 118 119
 FT STRAND 121 123
 FT SEQUENCE 123 AA; 13839 MW; 78598395FAE10257 CRC64;
 Query Match 35.0%; Score 43; DB 1; Length 123;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Qy 4 ASCHFGPLTWC 15
 | | | | |
 Db 95 ADCEIGPICGHC 106
 | | | | |
 RESULT 19
 MSS4_MOUSE
 ID MSS4_MOUSE STANDARD; PRT; 123 AA.
 AC Q91X36;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Guanine nucleotide exchange factor MSS4 (Rab interacting factor).
 GN RAB1F.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedini T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
 CC MEMBERS OF THE SEC4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
 CC FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
 CC THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
 CC TRANSPORT (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: BC011166; AAB11166.1; -;
 DR MCD: MGI-2138605; AW549708.
 DR Pfam: PF044421; Mss4; 1.
 KW Guanine-nucleotide releasing factor; Protein transport; Zinc.
 KM METAL 23 23 ZINC (BY SIMILARITY).
 FT TURN 23 23

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FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
SQ SEQUENCE 123 AA; 13915 MW; 733AECDDBE8B02 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 123;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
| | | | |
Db 95 ADCEIGPIGWHC 106
| | | | |

RESULT 20
MSS4_RAT STANDARD; PRT; 123 AA.
AC Q08326;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Guanine nucleotide exchange factor MSS4 (RAB interacting factor).
GN RABIF OR MSS4.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=10116;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA MEDLINE=93156814; PubMed=8429887;
RT "A mammalian guanine-nucleotide-releasing protein enhances function
of yeast secretory protein Sec4."
RL Nature 361:464-467(1993).
CC -!- FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON
MEMBERS OF THE SEC4/YPT1/RAB SUBFAMILY. STIMULATES GDP RELEASE
FROM BOTH YPT1 AND RAB3A, BUT IS LESS ACTIVE ON THESE PROTEINS
THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
TRANSPORT.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
CC
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CC
CC EMBL; X70496; CAA49904.1;
CC PIR; S29714; S29714.
CC PDB; 1HXR; 04-APR-01.
CC Pfam; PF04421; MSS4; 1.
KW Guanine-nucleotide releasing factor; Protein transport; Zinc;
3D-structure.
FT METAL 23 23 ZINC (BY SIMILARITY).
FT METAL 26 26 ZINC (BY SIMILARITY).
FT METAL 94 94 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT STRAND 11 11
FT TURN 13 14
FT STRAND 16 17
FT STRAND 21 23
FT TURN 24 26
FT STRAND 29 31
FT TURN 33 34
FT STRAND 37 39
FT STRAND 43 46
FT STRAND 49 50
FT HELIX 51 54
FT TURN 56 57
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FT STRAND 62 65
FT STRAND 68 71
FT HELIX 74 76
FT STRAND 81 82
FT STRAND 86 86
FT TURN 87 88
FT STRAND 89 93
FT TURN 95 97
FT TURN 99 100
FT STRAND 103 106
FT TURN 107 108
FT TURN 110 111
FT STRAND 113 116
FT HELIX 117 119
FT STRAND 120 123
SQ SEQUENCE 123 AA; 13928 MW; ACB7D07E2735811C CRC64;

Query Match 35.0%; Score 43; DB 1; Length 123;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
| | | | |
Db 95 ADCEIGPIGWHC 106
| | | | |

RESULT 21
PDX1_HUMAN STANDARD; PRT; 199 AA.
AC Q06830; P35703;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.1.1.1.-) (Thioredoxin dependent peroxidase 2) (Thioredoxin-dependent peroxide reductase 2) (Proliferation-associated protein PAG)
DE (Natural killer cell enhancing factor A) (NKEF-A).
GN PDX1 OR TDPX2 OR PAGB OR PAGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC MEDLINE=93266552; PubMed=8496166;
RA Prosperi M.T., Ferbus D., Karcinski I., Goubin G.;
RT "A human cDNA corresponding to a gene overexpressed during cell
proliferation encodes a product sharing homology with amoebic and
bacterial proteins."
RL J. Biol. Chem. 268:11050-11056(1993).
RN 2
RP SEQUENCE FROM N.A.
RC MEDLINE=94299283; PubMed=8026862;
RA Shau H., Butterfield L.H., Chiu R., Kim A.;
RT "Cloning and sequence analysis of candidate human natural killer-
enhancing factor genes."
RL Immunogenetics 40:129-134(1994).
RN 3
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Cabavant T.L., Scheetz T.E.,
Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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DE Nitrate transporter (Nitrate permease).
GN CRNA.
OS Emericella nidulans (Aspergillus nidulans).
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
CC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91095428; PubMed=1986367;
RA Unkles S.E., Hawker K.L., Grievé C., Campbell E.I., Montague P.,
RA Kinghorn J.R.;
RA "cDNA encodes a nitrate transporter in Aspergillus nidulans.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:204-208(1991);
RN [2]
RP ERMATUM
RA Unkles S.E., Hawker K.L., Grievé C., Campbell E.I., Montague P.,
RA Kinghorn J.R.;
RL Proc. Natl. Acad. Sci. U.S.A. 88:4564-4564(1991).
CC -!- FUNCTION: PERMEASE FOR NITRATE UPTAKE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- INDUCTION: SUBJECT TO NITRATE AND NITRITE INDUCTION, AND NITROGEN
CC METABOLITE REPRESSION. CNA EXPRESSION IS MEDIATED BY THE PRODUCTS
CC OF NIRA, AREA, AND NIAO.
CC
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CC
DR EMBL: M61125; AAA62125.1;
DR FMBL: U34382; AAA76713.1;
DR InterPro: IPR007114; NPS;
DR InterPro: IPR004737; NO3_transporter;
DR InterPro: IPR005828; Sub_transporter;
DR Pfam: PF00083; sugar_tr; 1;
DR TIGRFAMs: TIGR00886; 2A0108; 1;
KW Nitrate assimilation; Transport; Transmembrane.
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 35 55 POTENTIAL.
FT DOMAIN 56 71 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 72 92 POTENTIAL.
FT DOMAIN 93 100 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 101 121 POTENTIAL.
FT DOMAIN 122 130 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 131 151 POTENTIAL.
FT DOMAIN 152 161 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 162 182 POTENTIAL.
FT DOMAIN 183 198 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 199 219 POTENTIAL.
FT DOMAIN 220 306 CYTOPLASMIC (HYDROPHILIC) (POTENTIAL).
FT TRANSEM 307 327 POTENTIAL.
FT DOMAIN 328 357 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 358 378 POTENTIAL.
FT DOMAIN 379 389 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 390 410 POTENTIAL.
FT DOMAIN 411 417 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 418 438 POTENTIAL.
FT DOMAIN 439 507 CYTOPLASMIC (POTENTIAL).
FT SEQUENCE 507 AA; 54925 MW; 4A3D3FA643F16352 CRC64;
Query Match 35.0%; Score 43; DB 1; Length 507;
Best Local Similarity 47.4%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
QY 2 GTASCHFGPLTWCKPOGG 20
DB 354 GKWAAMFGFLNIVCRPAGG 372
RESULT: 24

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HUTU_HUMAN
ID HUTU_HUMAN STANDARD; PRT; 676 AA.
AC Q96N76;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable urocanate hydratase (EC 4.2.1.49) (Urocanase)
DE (Imidazolonepropionate hydrolase).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Osuki T., Sato H., Ota T., Wakamatsu A., Iehli S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Magatauma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuko Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-yl)propanoate = urocanate + H(2)O.
CC -!- COFACTOR: NAD (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AK055862; BAB71032.1;
DR GK: Q96N76;
DR MIW: 276880;
DR InterPro: IPR000193; Urocanase.
DR Pfam: PF01175; Urocanase; 1.
DR PRODOM: PD025423; Urocanase; 1.
DR PROSITE: PS01233; UROCANASE; 1.
KW Hypothetical protein; Histidine metabolism; Lyase; NAD.
SQ SEQUENCE 676 AA; 74830 MW; C940D3D068648D17 CRC64;
Query Match 35.0%; Score 43; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GGTSACHFGPLTWVC 15
DB 439 GDIFSQGGFPRWVC 453
RESULT 25
HUTU_MOUSE
ID HUTU_MOUSE STANDARD; PRT; 676 AA.
AC OBVC12;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable urocanate hydratase (EC 4.2.1.49) (Urocanase)
DE (Imidazolonepropionate hydrolase).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Zordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uzdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.L., Skalska U., Szallus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC -!- COPROANATE = UROCANATE + H2O.
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
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DR EMBL; BC022133; AAH22133.1; -;
DR InterPro: IPR000193; Urocanase.
DR Pfam: PF01175; Urocanase; 1.
DR ProDom: PD025423; Urocanase; 1.
DR TIGRFAMs: TIGR01228; hutU; 1.
DR PROSITE: PS01233; UROCANASE; 1.
KW Hypothetical protein; Histidine metabolism; Lyase; NAD.
SQ SEQUENCE 676 AA; 74590 MW; 6C8645F684E5455 CRC64;

Query Match 35.0%; Score 43; DB 1; Length 676;
Best Local Similarity 53.3%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVC 15
Db 439 GDIFSQGFPRWVC 453
|||||
[1]

RESULT 26
Y189 ARCFU STANDARD; PRT; 96 AA.
AC G30049;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AF0189.
GN AF0189
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kervlavage A.R., Graham D.E., Kyrpides N.C.,
RA Flickeimann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodex A., Zhou L.,
RA Overbeek R., Gocayne T.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
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DR EMBL; AF001093; AAB91047.1; -;
DR PIR: E69273; E69273.
DR TIGR: AF0189;
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 13 35 POTENTIAL.
SQ SEQUENCE 96 AA; 11332 MW; 22F660AA59C47795 CRC64;

Query Match 34.6%; Score 42.5; DB 1; Length 96;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 6 CHFGPLTWVC 15
Db 50 CHFRP-SWVC 58
|||||
[1]

RESULT 27
IF32 YEAST STANDARD; PRT; 347 AA.
AC P40217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 3 p39 subunit (eIF3 p39)
DE (Translation initiation factor eIF3, p39 subunit).
GN TIF34 OR YMR146C OR YMG375.16C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W303D;
RX MEDLINE=97127370; PubMed=8972194;
RA Naranda T., Kainuma M., Macmillan S.E., Hershey J.W.B.;
RT "The 39-kilodalton subunit of eukaryotic translation initiation
RT factor 3 is essential for the complex's integrity and for cell
RT viability in Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 17:145-153(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX PubMed=9169872;
RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule C., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrall B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93(1997).
CC -!- FUNCTION: EIF-3 DISSOCIATES RIBOSOMES, PROMOTES INITIATOR MET-TRNA
CC AND MRNA BINDING.

```
CC -- SUBUNIT: EIF-3 IS COMPOSED OF UP TO 8 DIFFERENT SUBUNITS.
CC -- SIMILARITY: Contains 5 WD repeats.
CC -----
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CC -----
DR EMBL; U56937; AAC49616.1; -
DR EMBL; Z47071; CA497361.1; -
DR PIR; S50403; S50403.
DR SGD; S2004754; TIF34.
DR GO; GO:0005852; C:eukaryotic translation initiation factor 3...; IDA.
DR GO; GO:0003743; P:translation initiation factor activity; IDA.
DR GO; GO:0006413; P:translational initiation; IDA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR ProDom; PDC00018; WD40; 5.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS00682; WD_REPEATS_2; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Initiation factor; Protein biosynthesis; Repeat; WD repeat.
FT REPEAT 8 38 WD 1.
FT REPEAT 50 80 WD 2.
FT REPEAT 149 181 WD 3.
FT REPEAT 194 224 WD 4.
FT REPEAT 291 321 WD 5.
SQ SEQUENCE 347 AA; 38755 MW; 56C0C09275B87622 CRC64;

Query Match: 34.68; Score 42.5; DB 1; Length 347;
Best Local Similarity 52.68; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

Qy 2 GTASCHFGPLTWVC-RPQ 19
Db 287 GRVQGHFGPLNTVAISPG 305

RESULT: 28
SEPA_HUMAN STANDARD; PR?; 478 AA.
AC C43236; Q9UM58;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Septin 4 (Peptide-like protein 2) [Brain protein H40 (Cell division
DE control-related protein 2) (hCDREL-2) (Bradykinin beta) (CE5B) beta)
DE (Cerebral protein-7) (hucep-7)].
GN SEPT4 OR PNUTL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RA Zha D., Hu G.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99107819; PubMed=9889007;
RA Paavola P., Horelli-Kuitunen N., Paolotte A., Pellonen J.;
RT "Characterization of a novel gene, PNUTL2, on human chromosome
RT 17q22-q23 and its exclusion as the Meckel syndrome gene.";
RL Genomics 55:122-125(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Brain;
RA Zieger B., Ware J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
KW Cell division; GTP-binding; Coiled coil; Alternative splicing.
```

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RN [4]
RP SEQUENCE FROM N.A.
RT TISSUE=Brain;
RA Tanaka M., Tanaka T., Kijima H., Itoh J., Matsuda T., Hori S.,
RA Yamamoto M.;
RT "Characterization of tissue- and cell-type-specific expression of a
RT novel human septin family gene, Bradykinin";
RL Biochem. Biophys. Res. Commun. 286:547-553(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A).
RT TISSUE=Brain;
RA Yoshimoto M., Yazaki M., Matsumoto K., Takayama K.;
RT "Molecular cloning of a new GTP binding protein from human brain.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM B).
RT TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibb R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -- FUNCTION: INVOLVED IN CYTOKINESIS (POTENTIAL).
CC -- SUBUNIT: MAY ASSEMBLE INTO A MULTICOMPONENT STRUCTURE.
CC -- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A;
CC Name=B;
CC IsoId=O43236-1; Sequence=Displayed;
CC IsoId=O43236-2; Sequence=VSP_006050;
CC -- SIMILARITY: BELONGS TO THE SEPTIN FAMILY.
CC -----
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CC -----
DR EMBL; AF035811; AAB88512.1; -
DR EMBL; AF073312; AAC25673.1; -
DR EMBL; U88829; AAD00653.1; -
DR EMBL; U88870; AAD00657.1; -
DR EMBL; AB008753; BAB70695.1; -
DR EMBL; D89278; BAB46922.1; -
DR EMBL; BC018056; AAL18056.1; -
DR Genbank; HGNC:9165; PNUTL2.
DR MIM; 603696; -
DR GO; GO:0003924; F:GTPase activity; TAS.
DR GO; GO:0005198; F:structural molecule activity; TAS.
DR GO; GO:0016288; P:cytokinesis; TAS.
DR InterPro; IPR000038; GTP_Cell_Div.
DR Pfam; PF00735; GTP_CDC; 1.
DR ProDom; PD002565; GTP_Cell_Div; 1.
KW Cell division; GTP-binding; Coiled coil; Alternative splicing.
```

FT NP BIND 151 158 GTP (POTENTIAL).
FT DOMAIN 447 478 COILED COIL (POTENTIAL).
FT VARSPIC 1 20 MBSLWQGNQSVPEKTEAG -> M (in isoform B).
FT /FTIGVSP 006050.
SQ SEQUENCE 478 AA: 55098 MW: 2F08D3611EF6523D CRC64;
Query Match 34.6%; Score 42.5; DB 1; Length 478;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 10; Conservative 1; Mismatches 4; Indels 5; Gaps 2;
Qy 2 GTASCHFGP---LTWVCKPQ 19
Db 43 GNASCH--PPEAKTWASRPQ 60
RESULT 29
PDX1_MOUSE STANDARD; PRT; 199 AA.
AC P35700;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.1) (Thioredoxin peroxidase 2) (Thioredoxin-
DE dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3)
DE (Macrophage 23 kDa stress protein).
GN PDX1 OR TDPX2 OR MSP23 OR PAGA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peritoneal macrophage;
RX MEDLINE=93366771; PubMed=8360158;
RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K.,
RA Sugita Y., Bannai S.;
RT "Cloning and characterization of a 23-kDa stress-induced mouse
Rt peritoneal macrophage protein";
RL J. Biol. Chem. 268:18633-18636(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Osteoblast;
RX MEDLINE=94375405; PubMed=8089076;
RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann E.;
RT "Cloning and characterization of OSF-3, a new member of the MERS
K. family, expressed in mouse osteoblastic cells.";
RL J. Biochem. 115:641-643(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RA Hino K., Sato H., Bannai S.;
RT "Characterization of mouse type I peroxiredoxin gun# and
Rt pseudogenes";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).
CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By
CC similarity). May form heterodimers with AOP2.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES; HIGH CONCENTRATION
CC IN LIVER.
CC -!- INDUCTION: BY OXIDATIVE AND SULFHYDRYL-REACTIVE AGENTS.
CC -!- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized
CC to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other
CC subunit to form an intermolecular disulfide with a concomitant
CC homodimer formation. The enzyme may be subsequently regenerated by
CC reduction of the disulfide by thioredoxin (By similarity).
CC -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52

(to Cys-SO3H) upon oxidative stress (By similarity).
CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC
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CC
CC EMBL; D16142; BAA03713.1; -
CC EMBL; D21252; BAA04796.1; -
CC EMBL; AB023564; BAA86992.1; -
CC EMBL; AB023560; BAA86992.1; JOINED.
CC EMBL; AB023561; BAA86992.1; JOINED.
CC EMBL; AB023562; BAA86992.1; JOINED.
CC EMBL; AB023563; BAA86992.1; JOINED.
CC PIR; A48513; A48513.
CC HSP; P30041; LPRX.
CC SWISS-2DPAGE; P35700; MOUSE.
CC MGD; MGI:99523; Pdx1.
CC GO; GO:0006979; P:response to oxidative stress; IDA.
CC InterPro; IPR000866; Ahpc-TSA.
CC Pfam; PF00578; Ahpc-TSA; 1.
CC Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT ACT_SITE 52 52 CYSTEINE SULFENIC ACID INTERMEDIATE
FT DISULFID 52 52 INTERCHAIN (WITH C-173) (IN
FT DISULFID 173 173 LINKED FORM) (BY SIMILARITY).
FT DISULFID 173 173 INTERCHAIN (WITH C-52) (IN
FT DISULFID 173 173 LINKED FORM) (BY SIMILARITY).
SQ SEQUENCE 199 AA; 22176 MW; B5F5C995A86124D1 CRC64;
Query Match 34.1%; Score 42; DB 1; Length 199;
Best Local Similarity 40.9%; Pred. No. 23;
Matches 9; Conservative 2; Mismatches 9; Indels 2; Gaps 1;
Qy 1 GGTASCHFGPGLTWVCKP--QGG 20
Db 75 GASVDSHFCHLAWINTPKQGG 96
RESULT 30
PDX1_RAT STANDARD; PRT; 199 AA.
AC Q63716;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Peroxiredoxin 1 (EC 1.11.1.1) (Thioredoxin peroxidase 2) (Thioredoxin-
DE dependent peroxide reductase 2) (Heme-binding 23 kDa protein) (HBP23).
GN PDX1 OR TDPX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96027454; PubMed=7577926;
RA Iwahara S.-I., Satoh H., Song D.-X., Webb J., Burlingame A.L.,
RA Nagae Y., Muller-Eberhard U.;
RT "Purification, characterization, and cloning of a heme-binding
RT protein (23 kDa) in rat liver cytosol";
RL Biochemistry 34:13398-13406(1995).
CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces
CC peroxides with reducing equivalents provided through the
CC thioredoxin system but not from glutaredoxin. May play an
CC important role in eliminating peroxides generated during
CC metabolism. Might participate in the signaling cascades of growth
CC factors and tumor necrosis factor-alpha by regulating the
CC intracellular concentrations of H(2)O(2).


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FT STRAND 190 191
FT TURN 198 199
FT STRAND 201 210
FT TURN 211 212
FT STRAND 224 225
SQ SEQUENCE 622 AA; 69505 MW; D97FD0328608C787 CRC64;

Query Match 34.1%; Score 42; DB 1; Length 622;
Best Local Similarity 77.8%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy 1 GGTASCHFG 9
|||
81 GGPNSCHFG 89

DE 81 GGPNSCHFG 89

RESULT 34
Y115 METJA
ID Y115_METJA STANDARD; PRT; 155 AA.
AC Q57579;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M30115.
GW M30115.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
CC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald T.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.L.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott C.L., Geohagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hannon M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
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CC -----
DR EMBL; M32882; AAA98256.1;
DR PIR; J03370; J03370.
DR InterPro; IPR002508; Amidase_3.
DR Pfam; PF01520; Amidase_3; 1.
DR SMART; SMO0646; Ami_3; 1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 342 AA; 38364 MW; BA9BBFCAE8EB135 CRC64;

Query Match 33.7%; Score 41.5; DB 1; Length 342;
Best Local Similarity 42.3%; Pred. No. 45;
Matches 11; Conservative 1; Mismatches 3; Indels 11; Gaps 2;

Qy 5 SCHF-----GPJ-----TWCKPQG 19
|||||
Db 75 S:HFDCYKDFDGLGTGTWCKEKG 100

RESULT 36
H1C1 MOUSE
ID H1C1_MOUSE STANDARD; PRT; 892 AA.
AC Q9RIY5; Q9RIY6; Q9RZ80;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hypermethylated in cancer 1 protein (Hic-1).
GN Hic1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A. AND DEVELOPMENTAL STAGE.
RC STRAIN=129/Sv. and Swiss Webster; TISSUE=Embryo;
RX MEDLINE=99172081; PubMed=10072440;
RA Grimm C., Spoerle R., Schmid T.E., Adler I.-D., Adamski J.,
RA Schughart K., Graw J.;
RT "Isolation and embryonic expression of the novel mouse gene Hic1, the
RT homologue of HIC1, a candidate gene for the Miller-Dieker syndrome.";
RL Hum. Mol. Genet. 8:697-710(1999).
RN 12;
RP SEQUENCE FROM N.A., DISEASE, AND TISSUE SPECIFICITY.
RX MEDLINE=20122251; PubMed=10655551;
RA Carter M.G., Johns M.A., Zeng X., Zhou L., Zink M.C., Mankowski J.L.,
RA Donovan D.M., Baylin S.B.;
RT "Mice deficient in the candidate tumor suppressor gene Hic1 exhibit
RT developmental defects of structures affected in the Miller-Dieker
RT syndrome."

```

Hum. Mol. Genet. 9:413-419(2000).
[3]
SEQUENCE OF 179-338 FROM N.A.
STRAIN=129/SV; TISSUE=Liver;
MEDLINE=99297610; PubMed=10371200;
Guertel C., Delcour S., Leprince D.;
"Evolutionary divergence in the broad complex, tramtrack and bric a
brac/poxviruses and zinc finger domain from the candidate tumor
suppressor gene hypermethylated in cancer.";
FEBS Lett. 451:253-256(1999).
-!- FUNCTION: Putative transcription factor. May act as a tumor
suppressor. May be involved in development of head, face, limbs
and ventral body wall.
-!- SUBUNIT: Interacts with CtBP (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms may be produced;
Name=1;
IsoId=Q9RLY5-1; Sequence=Displayed;
-!- TISSUE SPECIFICITY: Ubiquitously expressed with highest levels in
heart and lung.
-!- DEVELOPMENTAL STAGE: Expression is first detected in the embryo
after 9 dpc. In the embryo, expression is found in restricted
regions of somite derivatives, limb anlagen and cranio-facial
mesenchyme. In the fetus, it is additionally expressed in
mesenchymes apposed to precartilaginous condensations, at many
interfaces to budding epithelia of inner organs, and weakly in
muscles.
-!- DISEASE: Defects in HIC1 are the cause of perinatal death with
serious developmental anomalies, including acrania, exencephaly,
cleft palate, omphalocele, craniofacial and limb anomalies.
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
FINGER PROTEINS. HIC TRANSCRIPTION FACTORS SUBFAMILY.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
-!- SIMILARITY: Contains 5 C2H2-type zinc fingers.

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EMBL; AF036334; AAD30654.1; .
EMBL; AF036582; AAD30655.1; .
EMBL; AJ132691; CAB44493.1; .
HSSP; P08046; 1A1H.
MGD; MGI:1338010; Hic1.
InterPro; IPR000210; BTB_POZ.
InterPro; IPR007087; Znf_C2H2.
Pfam; PF00651; BTB; 1.
Pfam; PF00096; zf-C2H2; 5.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00225; BTB; 1.
SMART; SM00355; Znf_C2H2; 5.
PROSITE; PS00097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
MultiGene family; Nuclear protein; Transcription regulation;
DNA-binding; Zinc-finger; Metal-binding; Repeat;
Developmental protein; Alternative splicing.
DOMAIN 1 172 ARG/PRO/GLY-RICH.
FT DOMAIN 206 269
FT DOMAIN 271 278
FT DOMAIN 319 326 POLY-ALA.
FT DOMAIN 354 358 POLY-GLY.
FT ZN_FING 596 623 POLY-PRO.
FT ZN_FING 666 693 C2H2-TYPE 1.
FT ZN_FING 694 721 C2H2-TYPE 2.
FT ZN_FING 722 749 C2H2-TYPE 3.
FT ZN_FING 750 777 C2H2-TYPE 4.
FT ZN_FING 777 777 C2H2-TYPE 5.

FT SITE 400 404 BINDING TO CTBP.
SQ CONFLICT 242 242 N -> S (IN REF. 1; AAD30654).
SQ SEQUENCE 892 AA; 94320 MW; BBD16AA051995740 CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 892;
Best Local Similarity 47.6%; Pred. NO. 1.1e+02;
Matches 10; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
QY 1 GGTASCHFGPL-TWVCKPQG 20
Db 103 GRGSVCRFGPLQIRVCGKRG 123

RESULT 37
POL_HTLV2
ID POL_HTLV2 STANDARD; PRT; 982 AA.
AC P03363;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE POL polyprotein [Contains: Reverse transcriptase (EC 2.7.7.49);
DE Ribonuclease H (EC 3.1.26.4)].
OS Human T-cell leukemia virus type II (HTLV-II).
GN Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
OC NCBI_TaxID=11309;
RN SEQUENCE FROM N.A.
RX MEDLINE=85216449; PubMed=2582407;
RA Shimotohno K., Takahashi Y., Shimizu N., Gojobori T., Golde D.W.,
Chen I.-S.Y., Miwa M., Sugimura T.;
RT "Complete nucleotide sequence of an infectious clone of human T-cell
leukemia virus type II: an open reading frame for the protease
gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3101-3105(1985).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
phosphomonocester.
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ [DNA] (N).
CC -!- PTM: CLEAVAGE SITES THAT YIELD THE MATURE PROTEINS REMAIN TO BE
DETERMINED.
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EMBL; M10060; AAB59885.1; .
PIR; A03962; GNLIJH2.
HSSP; P03355; 1MML.
InterPro; IPR001037; Integrase_C.
InterPro; IPR003308; Integrase_Zn.
InterPro; IPR002156; RNaseH.
InterPro; IPR001584; RNe.
InterPro; IPR000477; RVTse.
Pfam; PF00552; Integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaase; 1.
Pfam; PF00665; rve; 1.
Pfam; PF00078; rvt; 1.
PolyProtein; Hydrolase; Endonuclease; Nuclease; Transferase;
RNA-directed DNA polymerase.
KW RNA-directed DNA polymerase.
SQ SEQUENCE 982 AA; 109853 MW; 3F97DD24229B931F CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 982;
Best Local Similarity 47.1%; Pred. NO. 1.2e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 3; Gaps 1;
QY 6 CHFGPLT---WVCKPQG 19
|::||| | | | |

```

Db      225 CNVPGTRYAVTVLPQG 241
RESULT 38
VGLM_HANTB STANDARD; PRT: 1133 AA.
AC P28728;
D 01-DEC-1992 (Rel. 24, Created)
D 01-DEC-1992 (Rel. 24, Last sequence update)
D 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Glycoprotein G1; Glycoprotein G2].
GN M.
OS Hantaan virus (strain B-1) [Korean hemorrhagic fever virus].
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=31617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370499; PubMed=2118626;
RA Isegawa Y., Fujiwara Y., Ohshima A., Fukutaga R., Murakami H.,
RA Yamanishi K., Sokawa Y.;
RT "Nucleotide sequence of the M genome segment of hemorrhagic fever
RT with renal syndrome virus strain B-1.",
RL Nucleic Acids Res. 18:4936-4936(1990).
CC -!- PPM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DE EMBL: X53861; GAA37854.1; --
DR PR: S12597; S12597.
DR InterPro: IPR002534; Hanta_G1.
DR InterPro: IPR002532; Hanta_G2.
DR Pfam: PF01567; Hanta_G1; 1.
DR Pfam: PF01561; Hanta_G2; 1.
DR Pfam: PF00096; zf-C2H2; 1.
DR ProDom: PD001813; Hanta_G2; 1.
DR Polyprotein; Glycoprotein; Transmembrane; Nonstructural protein;
KW Signal.
FT CHAIN 1 16 POTENTIAL.
FT CHAIN 17 1133 M POLYPROTEIN.
FT CHAIN 18 646 GLYCOPROTEIN G1.
FT CHAIN 647 1133 GLYCOPROTEIN G2.
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1133 AA; 125908 MW; 0A25160A32862FD6 CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1133;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
OY 3 TASCHFG-----PLTWVCKP 17
||| ||| :| |
746 TAKCFEKKDYENSWACNP 765
Db      246 TAKCFEKKDYENSWACNP 765
RESULT 39
VGLM_SEOUB STANDARD; PRT: 1133 AA.
AC P33455;
D 01-FEB-1994 (Rel. 28, Created)
D 01-FEB-1994 (Rel. 28, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN M.
OS Seoul virus (strain 80-39).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=12557;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91327730; PubMed=1867009;
RA Antic D., Lim B.U., Kang C.Y.;
RT "Molecular characterization of the M genomic segment of the Seoul
RT 80-39 virus; nucleotide and amino acid sequence comparisons with
RT other hantaviruses reveal the evolutionary pathway.",
RL Virus Res. 19:47-58(1991).
CC -!- PPM: SPECIFIC ENZYMOLOGICAL CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
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CC -----
DE EMBL: S47716; AAB19434.1; --
DR PR: A43964; A43964.
DR InterPro: IPR002534; Hanta_G1.
DR InterPro: IPR002532; Hanta_G2.
DR Pfam: PF01567; Hanta_G1; 1.
DR Pfam: PF01561; Hanta_G2; 1.
DR Pfam: PF00096; zf-C2H2; 1.
DR ProDom: PD001813; Hanta_G2; 1.
DR Polyprotein; Glycoprotein; Transmembrane; Nonstructural protein;
KW Signal.
FT CHAIN 1 17 POTENTIAL.
FT CHAIN 18 1133 M POLYPROTEIN.
FT CHAIN 18 646 GLYCOPROTEIN G1.
FT CHAIN 647 1133 GLYCOPROTEIN G2.
FT CARBOHYD 132 132 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1133 AA; 125775 MW; 3FD0695189E75DA9 CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1133;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
OY 3 TASCHFG-----PLTWVCKP 17
||| ||| :| |
746 TAKCFEKKDYENSWACNP 765
Db      746 TAKCFEKKDYENSWACNP 765
RESULT 40
VGLM_SEOUB STANDARD; PRT: 1133 AA.
AC P17880;
D 01-AUG-1990 (Rel. 15, Created)
D 01-AUG-1990 (Rel. 15, Last sequence update)
D 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polyprotein precursor [Contains: Glycoprotein G1; Glycoprotein G2].
GN M.
OS Seoul virus (strain SR-11) (Sapporo rat virus).

```


OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=11610;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 17-23 AND 647-654.
RX MEDLINE=90232720; PubMed=1970443;
SA Arikawa J., Lapenotiere H.F., Iacono-Connors L., Wang M.,
RA Schmaljohn C.S.;
RT "Coding properties of the S and the M genome segments of Sapporo rat
RT virus: comparison to other causative agents of hemorrhagic fever with
RT renal syndrome";
RL Virology 176:114-125(1990).
CC -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
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CC -----
DR EMBL: M34882; AAA47825.1; -
DR InterPro; IPR002534; Hanta_G1.
DR InterPro; IPR002534; Hanta_G2.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01567; Hanta_G1; 1.
DR Pfam; PF01561; Hanta_G2; 1.
DR ProDom; PD00096; zf-C2H2; 1.
DR ProDom; PD001813; Hanta_G2; 1.
KW Polypeptide; Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 1133 M POLYPROTEIN.
FT CHAIN 17 646 GLYCOPROTEIN G1.
FT CHAIN 647 1133 GLYCOPROTEIN G2.
FT TRANSMEM 444 461 POTENTIAL.
FT TRANSMEM 485 504 POTENTIAL.
FT TRANSMEM 625 646 POTENTIAL.
FT TRANSMEM 1105 1124 POTENTIAL.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1133 AA; 125591 MW; 81207219339A9E5B CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1133;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
Oy 3 TASCHFG-----PLTWVCKP 17
||| |||
Db 746 TAKCHFKEKYEYENSWACNP 765
RESULT 4:
VGLW SEQR
ID VGLW SEQR STANDARD; PRT; 1134 AA.
AC P28729;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE M polypeptide precursor [contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN M.
OS Secul virus (strain R22).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Hantavirus.
OX NCBI_TaxID=31620;
RN [1]
RP SEQUENCE FROM N.A.
SA Shi L.C., Hang C.S., Li D.X., Yuan J.S., Jin D.Y., Song G.;

RT "Molecular cloning and sequencing of the M genome segment of epidemic
RT hemorrhagic fever virus R22 strain.";
RL Ping Tu Heueh Pao 7:295-302(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92074322; PubMed=1962503;
RA Xu X.A., Ruo S.L., Tang Y.W., Fisher-Hoch S.P., McCormick J.B.;
RA "Molecular characterization and expression of glycoprotein gene of
RT Hantavirus R22 strain isolated from Rattus norvegicus in China.";
RL Virus Res. 21:35-52(1991).
CC -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
CC INCLUDING GLYCOPROTEIN G1 AND GLYCOPROTEIN G2.
CC -!- SIMILARITY: BELONGS TO THE HANTAVIRUSES M POLYPROTEIN FAMILY.
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CC -----
DR EMBL: S68035; AAB20470.2; -
DR PIR: JC1006; GNVU22.
DR InterPro; IPR002534; Hanta_G1.
DR InterPro; IPR002532; Hanta_G2.
DR Pfam; PF01567; Hanta_G1; 1.
DR Pfam; PF01561; Hanta_G2; 1.
DR ProDom; PD001813; Hanta_G2; 1.
KW Polypeptide; Glycoprotein; Transmembrane; Nonstructural protein;
Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 1134 M POLYPROTEIN.
FT CHAIN 17 646 GLYCOPROTEIN G1.
FT CHAIN 647 1134 GLYCOPROTEIN G2.
FT TRANSMEM 444 461 POTENTIAL.
FT TRANSMEM 485 504 POTENTIAL.
FT TRANSMEM 625 646 POTENTIAL.
FT TRANSMEM 1106 1125 POTENTIAL.
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 927 927 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 285 287 EEI -> KKF (IN REF. 2).
FT CONFLICT 645 645 S -> T (IN REF. 2).
FT CONFLICT 874 874 V -> D (IN REF. 2).
SQ SEQUENCE 1134 AA; 126319 MW; 60F4918FC42EE3ED CRC64;
Query Match 33.7%; Score 41.5; DB 1; Length 1134;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 5; Gaps 1;
Oy 3 TASCHFG-----PLTWVCKP 17
||| |||
Db 747 TAKCHFKEKYEYENSWACNP 766
RESULT 42
UNG CHLMU
ID UNG CHLMU STANDARD; PRT; 229 AA.
AC Q95J2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uracil-DNA glycosylase (EC 3.2.2.-) (UDG).
GN UNG OR TC0897.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.

```
RC STRAIN=MoPn / Nigg;
RA MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Winn M., Nelson W., DeBoer R., Kolaray J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae A39.";
RL Nucleic Acids Res. 28:1397-1406(2000);
CC -!- FUNCTION: Excises uracil residues from the DNA which can arise as
CC a result of misincorporation of dUMP residues by DNA polymerase or
CC due to deamination of cytosine (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC
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CC
CC EMBL; AE002356; AAP39691.1;
CC PIR; B81652; B81652.
CC HSSP; P12295; 1EUG.
CC TIGR; TC0897;
CC HAMAP; MF 00148; 1.
CC InterPro; IPR003249; U_glycylase_norp.
CC InterPro; IPR002043; UDNA_glycylase.
CC InterPro; IPR005122; UDNA_glycylaseSF.
CC Pfam; PF03167; UDG; 1.
CC ProDom; PD001589; U_glycylase_norp; 1.
CC TIGRFAMs; TIGR00628; ung; 1.
CC PROSITE; PS00130; U_DNA_GLYCOSYLASE; 1.
CC DNA repair; Hydrolase; Glycosidase; Complete proteome.
CC ACT SITE 70 70 GENERAL BASE (BY SIMILARITY).
CC SEQUENCE 229 AA; 25972 MW; C68786E753DBD9CA CRC64;
CC
CC Query Match 33.3%; Score 41; DB 1; Length 229;
CC Best Local Similarity 42.9%; Pred. No. 37;
CC Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 6 CHFGPLTWCKPOG 19
CC ||| : : : |||
CC Db 207 CHFSKINYLLKKQG 220
CC
CC RESULT 43
CC UNG_CHLTR STANDARD; PRT; 229 AA.
CC AC O84613;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Uracil-DNA glycosylase (EC 3.2.2.-) (UDG).
CC GN UNG CR CT507
CC OS Chlamydia trachomatis.
CC OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiales; Chlamydia.
CC OX NCBI_TaxID=813;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=D/UM-3/Cx;
CC RX MEDLINE=99000809; PubMed=9784136;
CC RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
CC Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
CC Davis R.W.;
CC RT "Genome sequence of an obligate intracellular pathogen of humans:
CC Chlamydia trachomatis.";
CC RL Science 282:754-759(1998).
CC -!- FUNCTION: Excises uracil residues from the DNA which can arise as
CC a result of misincorporation of dUMP residues by DNA polymerase or
```

```
CC due to deamination of cytosine (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC
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CC
CC EMBL; AE001331; AAC68210.1;
CC PIR; C71493; C71493.
CC HSSP; P12295; 1EUG.
CC HAMAP; MF 00148; 1.
CC InterPro; IPR003249; U_glycylase_norp.
CC InterPro; IPR002043; UDNA_glycylase.
CC InterPro; IPR005122; UDNA_glycylaseSF.
CC Pfam; PF03167; UDG; 1.
CC ProDom; PD001589; U_glycylase_norp; 1.
CC TIGRFAMs; TIGR00628; ung; 1.
CC PROSITE; PS00130; U_DNA_GLYCOSYLASE; 1.
CC DNA repair; Hydrolase; Glycosidase; Complete proteome.
CC ACT SITE 70 70 GENERAL BASE (BY SIMILARITY).
CC SEQUENCE 229 AA; 26002 MW; 9AD49846F8DCDC3B CRC64;
CC
CC Query Match 33.3%; Score 41; DB 1; Length 229;
CC Best Local Similarity 42.9%; Pred. No. 37;
CC Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 6 CHFGPLTWCKPOG 19
CC ||| : : : |||
CC Db 207 CHFSKINYLLKKQG 220
CC
CC RESULT 44
CC RNC_NEIMA STANDARD; PRT; 239 AA.
CC AC Q9JVD3;
CC DT 28-FEB-2003 (Rel. 41, Created)
CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Ribonuclease III (EC 3.1.26.3) (RNase III).
CC GN RNC OR NMA0888
CC OS Neisseria meningitidis (serogroup A)
CC OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
CC OC Neisseriaceae; Neisseria.
CC OX NCBI_TaxID=65699;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=22491 / Serogroup A / Serotype 4A;
CC RX MEDLINE=20222556; PubMed=10761919;
CC RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
CC Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
CC Davies R.M., Davis P., Davis K., Feltwell T., Hamlin N., Holroyd S.,
CC Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
CC Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
CC Whitehead S., Spratt B.G., Barrall B.G.;
CC RT "Complete DNA sequence of a serogroup A strain of Neisseria
CC meningitidis 22491.";
CC RL Nature 404:502-506(2000).
CC -!- FUNCTION: Digests double-stranded RNA. Involved in the processing
CC of ribosomal RNA precursors and of some mRNAs (By similarity).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Contains 1 DBM (double-stranded RNA-binding) domain.
CC -!- SIMILARITY: Contains 1 DBM III domain.
CC
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2R TIGR00552, made; 1.
KW Ligase; NAD; ATP-binding; Complete proteome.
FT NP BIND 30 37 ATP (BY SIMILARITY).
FT ACT SITE 32 32 BY SIMILARITY.
SQ SEQUENCE 248 AA; 28189 MW; 45E43C687545220E CRC64;

Query Match 33.3%; Score 41; DB 1; Length 248;
Best Local Similarity 40.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 7; Indels 0;
Gaps 0;
2 GTASCHFGPLTWCK 16
149 GDGACDIAPLAWLK 163

RESULT 47

CYCFC_RHOSH
ID CYCFC_RHOSH STANDARD; PRT; 296 AA.
AC Q53143;
DT 01-NOV-1997 (Rel. 35, Created);
DT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Diheme cytochrome C-type.
GN CYCFC.
OS Rhodobacter sphaeroides [Rhodospirillum rubrum] sphaeroides.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
CC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=95362655; PubMed=7543472;
RA Flory J.E., Donohue T.J.;
RT "Organization and expression of the Rhodobacter sphaeroides cyfc operon";
RT J. Bacteriol. 177:4311-4320(1995).
CC -!- FUNCTION: DIHEME C-TYPE CYTOCHROME, THAT IS PARTICULARLY EXPRESSED WHEN CELLS GENERATE ENERGY VIA AEROBIC RESPIRATION.
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC -!- PTM: BINDS TWO HEME GROUPS PER MOLECULE (POTENTIAL).
CC -!- SIMILARITY: TO ACETOBACTER ALCOHOL DEHYDROGENASE CYTOCHROME C SUBUNIT.
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EMBL; L36880; AA009146.1; -
DR InterPro: IPR003088; Cyt C.
DR InterPro: IPR003219; CytC adh.
DR InterPro: IPR000345; CytC heme bind.
DR Pfam: PF00034; Cytochrome-C_1.
DR ProDom: PD011584; CytC adh_1.
DR PROSITE; PS00190; CYTOCHROME C; 2.
KW Electron transport; Heme; Membrane.
FT BINDING 52 52 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 55 55 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 56 56 IRON (HEME 1 AXIAL LIGAND) (BY SIMILARITY).
FT METAL 56 56 IRON (HEME 1 AXIAL LIGAND) (BY SIMILARITY).
FT BINDING 202 202 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 205 205 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 206 206 IRON (HEME 2 AXIAL LIGAND) (BY SIMILARITY).
FT METAL 206 206 IRON (HEME 2 AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 296 AA; 31727 MW; 4CA9D8F69585BFD CRC64;

Query Match 33.3%; Score 41; DB 1; Length 296;
Best Local Similarity 70.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTSCHFGSP 10
DB 50 GGCASCHAAP 59
RESULT 48
TLX1_HUMAN
ID TLX1_HUMAN STANDARD; PRT; 330 AA.
AC P31314; O75699; OHCA0;
DT 01-JUL-1993 (Rel. 26, Created);
DT 01-JUL-1993 (Rel. 26, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE T-cell leukemia homeobox protein 1 (Homeobox protein Hox-11) (TCL-3 proto-oncogene).
GN TLX1 OR HOX11 OR TCL3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020958; PubMed=1681546;
RA Kennedy M.A., Gonzalez-Sarmiento R., Kees U.R., Lampert F., Dear T.N., Boehm T., Rabbitts T.H.;
RT "HOX11, a homeobox-containing T-cell oncogene on human chromosome 10q24";
RT Proc. Natl. Acad. Sci. U.S.A. 88:8900-8904(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92007734; PubMed=1717256;
RA Lu M., Gong Z., Shen W., Ho A.D.;
RT "The tcl-3 proto-oncogene altered by chromosomal translocation in T-cell leukemia codes for a homeobox protein";
RT EMBO J. 10:2905-2910(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319541; PubMed=1352396;
RA Lu M., Zhang N., Ho A.D.;
RT "Genomic organization of the putative human homeobox proto-oncogene HOX-11 (TCL-3) and its endogenous expression in T cells";
RT Oncogene 7:1325-1330(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91289163; PubMed=1676542;
RA Hatano M., Roberts C.W., Minden M., Crist W.M., Korsmeyer S.J.;
RT "Deregulation of a homeobox gene, HOX11, by the t(10;14) in T cell leukemia";
RT Science 253:79-82(1991).
RN [5]
RP SEQUENCE FROM N.A.
RA Watt P.M., Rarford P.R., Kees U.R.;
RT "HUG-1: a novel upstream gene neighboring HOX11 at 10q24 is expressed in a T-cell leukaemia cell line";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-64 FROM N.A.
RX MEDLINE=98449474; PubMed=9778044;
RA Brake R.L., Kees U.R., Watt P.M.;
RT "Multiple negative elements contribute to repression of the HOX11 proto-oncogene";
RL Oncogene 17:1787-1795(1998).
CC -!- FUNCTION: CONTROLS THE GENESIS OF THE SPLEEN. BINDS TO THE DNA SEQUENCE 5'-GGCGTAAGTG-3'.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(10;14)(Q24;Q11) WHICH INVOLVES HOX11 AND T-CELL RECEPTOR DELTA CHAIN (TCRD) GENES.
CC -!- SIMILARITY: Contains 1 homeobox domain.
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CC -----
DR EMBL; M75952; AAA58662.1; -;
DR EMBL; M62626; AAA36719.1; -;
DR EMBL; S38742; AAB19293.1; -;
DR EMBL; AJ009794; CAA08834.1; -;
DR EMBL; AF067443; AAG10096.1; -;
DR PIR; A40855; A40855;
DR HSSP; P14653; 1B72.
DR TRANSFAC; T02054; -;
DR Genew; HGNC:5056; TLX1.
DR MIM; 186770; -;
DR GO; GO:0007048; P:oncogenesis; TAS.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PDC00010; Homeobox; 1.
DR SMART; SM00389; Hox; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX-2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Developmental protein;
KW Proto-oncogene; Chromosomal translocation.
FT DNA BIND 201 260 HOMEBOX.
FT CONFLICT 71 71 A -> T (IN REF. 5).
FT CONFLICT 276 276 L -> R (IN REF. 4).
SQ SEQUENCE 330 AA; 34365 MW; 09A518FB5271F7ED CRC64;

Query Match 33.3%; Score 41; DB 1; Length 330;
Best Local Similarity 58.3%; Pred. No. 52;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 GGTASCHFGPLT 12
DB 87 GGGACSMGPLT 98

RESULT 49

DR ORYB ORYSA STANDARD; PRT; 471 AA.
AC P2577;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
L1 15-SEP-2003 (Rel. 42, Last annotation update)
DE Oryza sativa beta chain precursor (EC 3.4.22.-).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
[1]
PP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare; TISSUE=Seed;
RX MEDLINE=91350494; PubMed=1885617;
RA Watanabe H., Abe K., Emori Y., Hosoyama H., Arai S.;
RT "Molecular cloning and gibberellin-induced expression of multiple
cysteine proteinases of rice seeds (oryzains).";
RL J. Biol. Chem. 266:16897-16902(1991).
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN SEEDS.
CC -!- INDUCTION: By gibberellic acid (GA).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL; D90407; BAA14403.1; -;
DR PIR; JU0389; KHRZOB.

DR PDB; 1FWO; 09-MAY-01.
DR MEROPS; C01.029; -;
DR Gramene; P25777; -;
DR InterPro; IPR000118; Granulin.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000169; SHprot_acSite.
DR Pfam; PF00396; granulin; 1.
DR Pfam; PF00112; Peptidase_C1; 1.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00277; GRAN; 1.
DR SMART; SM00645; Pept C1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Thiol protease; Zymogen; Glycoprotein; Signal;
KW 3D-structure.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 139 ACTIVATION PEPTIDE (POTENTIAL).
FT CHAIN 140 471 ORYZAIN BETA CHAIN.
FT ACT_SITE 164 164 BY SIMILARITY.
FT ACT_SITE 301 301 BY SIMILARITY.
FT ACT_SITE 321 321 BY SIMILARITY.
FT DISULFID 161 204 BY SIMILARITY.
FT DISULFID 195 237 BY SIMILARITY.
FT DISULFID 295 346 BY SIMILARITY.
FT CARBOHYD 340 340 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 471 AA; 50505 MW; 0BF39D33995CEBID CRC64;

Query Match 33.3%; Score 41; DB 1; Length 471;
Best Local Similarity 41.7%; Pred. No. 72;
Matches 10; Conservative 0; Mismatches 10; Indels 4; Gaps 1;

OY 1 GGTASCHFG----PLTWCKPQGG 20
DB 394 GSTCCCAFGRNLCVWGCCPVEG 417

RESULT 50

DR AD15 HUMAN STANDARD; PRT; 814 AA.
AC Q13474; Q13493; O96C78;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-
rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
DE (Metargidin).
GN ADAM15 OR MDC15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
PP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=96214870; PubMed=8617717;
RA Kraetzschmar J., Lum L., Blobel C.P.;
RT "Metargidin, a membrane-anchored metalloprotease-disintegrin protein
with an RGD integrin binding sequence.";
RL J. Biol. Chem. 271:4593-4596(1996).
[2]
PP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=97192141; PubMed=9039960;
RA Herren B., Raines E.W., Ross R.;
RT "Expression of a disintegrin-like protein in cultured human vascular
cells and in vivo.";
RL FASEB J. 11:173-180(1997).
[3]
PP SEQUENCE FROM N.A.
RC Karkkainen I., Huovila A.-P.J.;

"The characterization of human ADAM15 gene structure and promoter region."
Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
(4)

SEQUENCE FROM N.A.

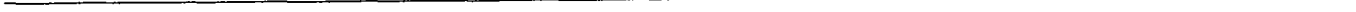
RT MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derce J.G.,
RA Klausberg R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko I., Xarusina K., Farmer A.A., Rubin G.M., Hong E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalon D.K., McNzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[5]
RP INTERACTION WITH INTEGRIN ALPHA-V-BETA3.
RX MEDLINE=98184837; PubMed=9516430;
RA Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., Takada Y.,
RT "Specific interaction of the recombinant disintegrin-like domain of
RT MDC-15 (metaraglin, ADAX-15) with integrin alphavbeta3.";
RJ J. Biol. Chem. 273:7345-7350(1998).
[6]
RP PHOSPHORYLATION OF TYR-715 AND TYR-735.
RX MEDLINE=21826475; PubMed=1741929;
RA Poghosyan Z., Robbins S.M., Houslay M.D., Webster A., Murphy G.,
RA Edwards D.R.;
RT "Phosphorylation-dependent interactions between ADAM15 cytoplasmic
RT domain and Src family protein-tyrosine kinases.";
RJ J. Biol. Chem. 277:4999-5007(2002).
CC -!- FUNCTION: May be involved in cell-surface proteolysis, cell
CC adhesion or intracellular protein maturation.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (by similarity).
CC -!- SUBUNIT: Interacts with ITGA9-ITGB3 (with integrin receptor),
CC PACSIN3 and SNX9. PACSIN3 and SNX9 preferentially bind the
CC precursor but not the processed form of ADAM15, suggesting that
CC the interaction occurs in a secretory pathway compartment prior to
CC the medial Golgi. (By similarity). Interacts specifically with Src
CC family protein-tyrosine kinases (PTKs).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. OVEREXPRESSED IN
CC ARTEROSCLEROTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTURED
CC ENDOTHELIAL AND SMOOTH MUSCLE.
CC -!- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
CC SORTING NEXIN 9 (BY SIMILARITY).
CC -!- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3.
CC -!- PTM: THE PRECURSOR IS CLEAVED BY A FUZIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -!- PTM: Phosphorylation increases association with PTKs.
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC
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DR EMBL; U46005; AAC51112.1; --
DR EMBL; U41767; AAC50404.1; --
DR EMBL; AF314227; AAM41189.1; --
DR EMBL; BC014566; AAH14566.1; --
DR HSSP; P18619; IFVL. --
DR MEROPS; M12.215; --
DR Genew; HGNC:193; ADAM15.
DR MW; 605548; --
GO; GO:0007160; P-cell-matrix adhesion; TAS.
DR InterPro; IPR006586; ADAM Cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001818; Matrxin.
DR InterPro; IPR002870; Pep M12B proppe.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn MTpeptdse.
DR Pfam; PF00220; disintegrin; 1.
DR Pfam; PF01582; Pep_M12B_proppe; 1.
DR Pfam; PF01421; Repolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SMC0608; ACR; 1.
DR SMART; SMC0050; DISIN; 1.
DR PROSITE; PS00215; ADAM_MEPRO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
KW Hydrolase; Metalloprotease; Zinc; Signal; Glycoprotein; Zymogen;
KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
FT SIGNAL 1 17 POTENTIAL.
FT PROPEP 18 206 BY SIMILARITY.
FT CHAIN 207 814 ADAM 15.
FT DOMAIN 207 696 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 697 717 POTENTIAL.
FT DOMAIN 718 814 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 207 414 METALLOPROTEASE.
FT DOMAIN 421 508 DISINTEGRIN-LIKE.
FT DOMAIN 509 656 CYS-RICH.
FT DOMAIN 657 685 EGF-LIKE.
FT SITE 766 772 SH3-BINDING (POTENTIAL).
FT SITE 801 807 SH3-BINDING (POTENTIAL).
FT SITE 179 179 CYSTEINE SWITCH (POTENTIAL).
FT SITE 484 486 CELL ATTACHMENT SITE (POTENTIAL).
FT METAL 348 348 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 349 349 BY SIMILARITY.
FT METAL 352 352 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 358 358 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 323 409 BY SIMILARITY.
FT DISULFID 480 493 POTENTIAL.
FT DISULFID 657 667 BY SIMILARITY.
FT DISULFID 661 673 BY SIMILARITY.
FT DISULFID 675 684 BY SIMILARITY.
FT MOD RES 715 715 PHOSPHORYLATION.
FT MOD RES 735 735 PHOSPHORYLATION.
FT CARBOHYD 237 237 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 714 714 S -> G (IN REF. 1).
FT CONFLICT 791 791 A -> P (IN REF. 2).
SQ SEQUENCE 814 AA; 87716 MW; 683A8368AD30996B CRC64;

Query Match 33.3%; Score 41; DB 1; Length 814;
Best Local Similarity 37.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Oy 5 SCHFGPLTWCKPQGG 20
Db 470 NCQURPSGWCQRPTRG 485

Search completed: November 5, 2003, 19:05:56
Job time : 13 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 5, 2003, 19:03:28 ; Search time 34 seconds
(without alignments)

151.796 Million cell updates/sec

Title: US-09-863-600E-19

Perfect score: 123

Sequence: 1 GGTASCHFGPLTWCKPQGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virue.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	50.5	41.1	155	17	Q53320	Q53320 methanobact
2	49	39.8	240	17	Q97AQ2	Q97AQ2 thermoplasm
3	49	39.8	499	3	Q02733	Q02733 saccharomyc
4	48.5	39.4	519	11	Q8B350	Q8B350 mus musculu
5	48.5	39.4	572	11	Q8BGV5	Q8BGV5 mus musculu
6	48	39.0	241	5	Q9V6U3	Q9V6U3 drosophila
7	48	39.0	852	10	Q9LI18	Q9LI18 oryza sativ
8	47	38.2	68	2	Q53375	Q53375 synechococc
9	47	38.2	209	16	Q8EJ61	Q8EJ61 shewanella
10	47	38.2	319	10	Q9M218	Q9M218 arabidopsis
11	47	38.2	324	10	Q9C5E4	Q9C5E4 arabidopsis
12	47	38.2	440	11	Q8CC47	Q8CC47 mus musculu
13	47	38.2	520	11	Q9JHX9	Q9JHX9 mus musculu
14	47	38.2	520	11	Q99KU8	Q99KU8 mus musculu
15	47	38.2	689	5	O01545	O01545 caenorhabdi
16	47	38.2	694	10	Q9FHJ8	Q9FHJ8 arabidopsis

17	47	38.2	695	10	Q9SLT7	Q9SLT7 arabidopsis
18	47	38.2	871	10	Q9LQ54	Q9LQ54 arabidopsis
19	47	38.2	2327	13	Q91BG7	Q91BG7 xenopus lae
20	46.5	37.8	641	11	Q8BVW2	Q8BVW2 mus musculu
21	46	37.4	94	10	Q9FQ67	Q9FQ67 helianthus
22	46	37.4	240	1	Q08710	Q08710 thermoplasm
23	46	37.4	240	17	Q9HJG6	Q9HJG6 thermoplasm
24	46	37.4	270	2	O33722	O33722 spirulina p
25	46	37.4	272	16	O44502	O44502 anabaena sp
26	46	37.4	347	5	O45177	O45177 caenorhabdi
27	46	37.4	1627	10	Q8GU51	Q8GU51 oryza sativ
28	45.5	37.0	286	10	Q9LT12	Q9LT12 arabidopsis
29	45.5	37.0	289	16	Q8X232	Q8X232 ralonstia s
30	45.5	37.0	323	16	Q8X233	Q8X233 ralonstia s
31	45.5	37.0	356	10	Q9LT13	Q9LT13 arabidopsis
32	45.5	37.0	494	4	O95965	O95965 homo sapien
33	45.5	37.0	494	11	Q8VDV0	Q8VDV0 mus musculu
34	45.5	37.0	548	4	Q8N172	Q8N172 homo sapien
35	45	36.6	79	12	Q8QUU9	Q8QUU9 infectious
36	45	36.6	220	16	Q8YSR8	Q8YSR8 anabaena sp
37	45	36.6	254	11	Q8K4K8	Q8K4K8 mus musculu
38	45	36.6	277	2	O07873	O07873 synechococc
39	45	36.6	338	10	Q8LAH5	Q8LAH5 arabidopsis
40	45	36.6	370	16	Q9RRJ7	Q9RRJ7 deinococcus
41	45	36.6	373	10	Q8LJ56	Q8LJ56 chlamydomon
42	45	36.6	534	10	Q9LGI2	Q9LGI2 oryza sativ
43	45	36.6	1225	12	Q91IE0	Q91IE0 lymantria d
44	45	36.6	1225	12	Q8B976	Q8B976 dendrolimus
45	45	36.6	1290	16	Q8YSJ3	Q8YSJ3 anabaena sp
46	45	36.6	1494	10	Q8H5A7	Q8H5A7 oryza sativ
47	45	36.6	1622	10	Q9C8G9	Q9C8G9 arabidopsis
48	45	36.6	1622	10	O24635	O24635 arabidopsis
49	45	36.6	2910	5	Q26008	Q26008 plasmodium
50	45	36.6	2914	5	Q8I410	Q8I410 plasmodium
51	44.5	36.2	210	11	Q8BKJ4	Q8BKJ4 mus musculu
52	44.5	36.2	494	11	Q8BMS0	Q8BMS0 mus musculu
53	44.5	36.2	1321	12	Q8BEM8	Q8BEM8 callitrichi
54	44	35.8	158	16	Q8XSV7	Q8XSV7 ralonstia s
55	44	35.8	180	2	O82968	O82968 ralonstia s
56	44	35.8	209	12	Q8QTY4	Q8QTY4 foot-and-mo
57	44	35.8	314	12	Q84584	Q84584 paramecium
58	44	35.8	338	10	Q93Y57	Q93Y57 arabidopsis
59	44	35.8	338	10	Q9LY31	Q9LY31 arabidopsis
60	44	35.8	374	2	Q8GLI2	Q8GLI2 bacillus ha
61	44	35.8	388	16	Q9KB30	Q9KB30 bacillus ha
62	44	35.8	422	4	Q81XW4	Q81XW4 homo sapien
63	44	35.8	435	13	Q9PUJ6	Q9PUJ6 carassius a
64	44	35.8	608	16	Q8DSU9	Q8DSU9 vibrio vuln
65	44	35.8	628	3	Q96X54	Q96X54 aspergillus
66	44	35.8	628	3	Q8NK90	Q8NK90 aspergillus
67	44	35.8	733	16	Q8U5X5	Q8U5X5 agrobacteri
68	44	35.8	1539	10	Q41813	Q41813 zea mays (m
69	43.5	35.4	482	10	Q8RV20	Q8RV20 oryza sativ
70	43.5	35.4	1284	16	Q98DC9	Q98DC9 rhizobium l
71	43	35.0	106	16	Q8NQV6	Q8NQV6 corynebacte
72	43	35.0	119	16	Q8U856	Q8U856 agrobacteri
73	43	35.0	205	12	Q8BEF8	Q8BEF8 foot-and-mo
74	43	35.0	209	12	Q8QTX5	Q8QTX5 foot-and-mo
75	43	35.0	210	12	Q8QTY2	Q8QTY2 foot-and-mo
76	43	35.0	210	12	Q8BEE8	Q8BEE8 foot-and-mo
77	43	35.0	211	12	Q8QTX2	Q8QTX2 foot-and-mo
78	43	35.0	211	12	Q8QTY0	Q8QTY0 foot-and-mo
79	43	35.0	211	12	Q8QTX9	Q8QTX9 foot-and-mo
80	43	35.0	211	12	Q9JDX3	Q9JDX3 foot-and-mo
81	43	35.0	211	12	Q8BEF5	Q8BEF5 foot-and-mo
82	43	35.0	211	12	Q8BEF1	Q8BEF1 foot-and-mo
83	43	35.0	211	12	Q8BEE1	Q8BEE1 foot-and-mo
84	43	35.0	211	12	Q8BED0	Q8BED0 foot-and-mo
85	43	35.0	211	12	Q8BEC5	Q8BEC5 foot-and-mo
86	43	35.0	211	12	Q8BEC0	Q8BEC0 foot-and-mo
87	43	35.0	211	12	Q8BEB9	Q8BEB9 foot-and-mo
88	43	35.0	211	12	Q8BEB2	Q8BEB2 foot-and-mo
89	43	35.0	211	12	Q8BEB1	Q8BEB1 foot-and-mo

RESULT 7					
ID	Q9L118	PRELIMINARY;	PRT;	852 AA.	
AC	Q9L118;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	EST AU057816(S21817) corresponds to a region of the predicted gene.				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophytes; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
OX	Ehrhartioideae; Oryzoaceae; Oryza.				
OX	NCBI_TaxID=4530;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. Nipponbare;				
RC	Sasaki T., Matsumoto T., Yamamoto K.;				
RA	"Oryza sativa nipponbare(Gam3) genomic DNA, chromosome 1, PAC clone:P0708G02.";				
RL	Submitted (MAR-2000) to the ENSEMBL/GenBank/DBJ databases.				
DR	EMBL: AP001539; BAA2920.1; -;				
DR	Graeme; Q9L118; -;				
DR	InterPro; IPR000270; OPR Pbl.				
DR	InterPro; IPR003035; RWP-RK.				
DR	Pfam; PF00564; Pbl; 1.				
DR	Pfam; PF02042; RWP-RK; 1.				
DR	SMART; SM00666; Pbl; 1.				
SQ	SEQUENCE 852 AA; 94146 MW; 3F8512886220B970 CRC64;				
Query Match 39.0%; Score 48; DB 10; Length 852;					
Best Local Similarity 62.5%; Pred. No. 51;					
Matches 10; Conservative 1; Mismatches 3; Indels 2					
QY	4 ASCHFGPL--TWCKP 17	:			
DB	678 ASCHGSPPANTFVCKP 693	:			
RESULT 8					
ID	Q53375	PRELIMINARY;	PRT;	68 AA.	
AC	Q53375;				
DT	01-NOV-1996 (TrEMBLrel. 01, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)				
DE	URF 10.				
OS	Synechococcus sp. (strain PCC 6716).				
OC	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.				
OX	NCBI_TaxID=32048;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=6716;				
RC	MEDLINE=93371369; PubMed=8363578;				
RA	van Walraven H.S., Lutter R., Walker J.E.;				
RT	"Organization and sequences of genes for the subunits of ATP synthase in the thermophilic cyanobacterium Synechococcus 6716.";				
RL	Biochem J 294:239-251(1993).				
DR	EMBL; X70432; CAA49886.1; -;				
FT	CHAIN 2 68				
SQ	SEQUENCE 68 AA; 7520 MW; 77653F692DCC9D9 CRC64;				
Query Match 38.2%; Score 47; DB 2; Length 68;					

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Best Local Similarity 50.0%; Pred. NO. 5.9;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
   | : | | | | |
Db 8 GNSMSMTGPITWIKP 23

RESULT 9
Q8EJ61
Q8EJ61

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ID Q8EJ61 PRELIMINARY; PRT: 209 AA.
AC Q8EJ61;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Stringent starvation protein a.
GN SSPA OR SO0611.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368913;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Mathe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Seaman M., Brinkac L., Daugherty S.,
RA DeSoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolchak J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
RA Feilblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AF015508; AAN53689.1; -.
DR TIGR; SO0611; -.
KW Complete proteome.
SQ SEQUENCE 209 AA; 24081 MW; 56846672B8767E52 CRC64;

Query Match 38.2%; Score 47; DB 16; Length 209;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTW 13
Db 153 GLADCYLGPLLW 164

RESULT 10
Q9W218 PRELIMINARY; PRT: 319 AA.
AC Q9W218;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical 34.4 kDa protein.
GN T8B10 70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138646; CAB81827.1; -.
KW Hypothetical protein.
SQ SEQUENCE 319 AA; 34419 MW; ACAB300D6FC9707D CRC64;

Query Match 38.2%; Score 47; DB 10; Length 319;
Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTASCHFGPLTWCKP 18
Db 153 GLADCYLGPLLW 164

RESULT 11
Q9C5E4 PRELIMINARY; PRT: 324 AA.
ID Q9C5E4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 35.1 kDa protein.
GN T8B10_70/AT3G60410.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T8B10_70/AT3G60410 (GI:7287989).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360301; AAK26011.1; -.
KW Hypothetical protein.
FT VARIANT 47 47 P -> L.
SQ SEQUENCE 324 AA; 35053 MW; 4DADC919C11CAD8E CRC64;

Query Match 38.2%; Score 47; DB 10; Length 324;
Best Local Similarity 44.4%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTASCHFGPLTWCKP 18
Db 188 GGOEADFGPKTNLRPR 205

RESULT 12
Q8CC47 PRELIMINARY; PRT: 440 AA.
ID Q8CC47;
AC Q8CC47;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical 34.4 kDa protein.
GN T8B10 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).";
DR EMBL; AK033946; BAC28521.1; -.
SQ SEQUENCE 440 AA; 48556 MW; A750CD5783AF02D4 CRC64;

Query Match 38.2%; Score 47; DB 11; Length 440;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 158 GSPNCHFGPYDNKAP 173
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ID Q8EJ61 PRELIMINARY; PRT: 209 AA.
AC Q8EJ61;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Stringent starvation protein a.
GN SSPA OR SO0611.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368913;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Mathe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Seaman M., Brinkac L., Daugherty S.,
RA DeSoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolchak J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,
RA Feilblyum T.V., Smith H.O., Venter J.C., Neelson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AF015508; AAN53689.1; -.
DR TIGR; SO0611; -.
KW Complete proteome.
SQ SEQUENCE 209 AA; 24081 MW; 56846672B8767E52 CRC64;

Query Match 38.2%; Score 47; DB 16; Length 209;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTW 13
Db 153 GLADCYLGPLLW 164

RESULT 10
Q9W218 PRELIMINARY; PRT: 319 AA.
AC Q9W218;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Hypothetical 34.4 kDa protein.
GN T8B10 70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138646; CAB81827.1; -.
KW Hypothetical protein.
SQ SEQUENCE 319 AA; 34419 MW; ACAB300D6FC9707D CRC64;

Query Match 38.2%; Score 47; DB 10; Length 319;
Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTASCHFGPLTWCKP 18
Db 153 GLADCYLGPLLW 164

RESULT 11
Q9C5E4 PRELIMINARY; PRT: 324 AA.
ID Q9C5E4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 35.1 kDa protein.
GN T8B10_70/AT3G60410.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Full length cDNA of gene T8B10_70/AT3G60410 (GI:7287989).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF360301; AAK26011.1; -.
KW Hypothetical protein.
FT VARIANT 47 47 P -> L.
SQ SEQUENCE 324 AA; 35053 MW; 4DADC919C11CAD8E CRC64;

Query Match 38.2%; Score 47; DB 10; Length 324;
Best Local Similarity 44.4%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GTASCHFGPLTWCKP 18
Db 188 GGOEADFGPKTNLRPR 205

RESULT 12
Q8CC47 PRELIMINARY; PRT: 440 AA.
ID Q8CC47;
AC Q8CC47;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical 34.4 kDa protein.
GN T8B10 70.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573 (2002).";
DR EMBL; AK033946; BAC28521.1; -.
SQ SEQUENCE 440 AA; 48556 MW; A750CD5783AF02D4 CRC64;

Query Match 38.2%; Score 47; DB 11; Length 440;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
Db 158 GSPNCHFGPYDNKAP 173
```

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RESULT 13
Q9JHK9 PRELIMINARY; PRT; 520 AA.
ID Q9JHK9
AC Q9CHK9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE N-acetyl-galactosamine-6-sulfate sulfatase.
GN GALNS.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ, and C57BL/6J.
RX MEDLINE=20164110; PubMed=1069374;
RA Montano A.M., Yamagishi A., Tomatsu S., Fukuda S., Copeland N.G.,
RA Orii K.E., Isogai K., Yamada N., Kato Z.I., Jenkins N.A.,
RA Gilbert D.J., Sukegawa K., Orii T., Kondo N.;
RT "The mouse N-acetyl-galactosamine-6-sulfate sulfatase (GALNS) gene:
RT cDNA isolation, genomic characterization, chromosomal assignment and
RT analysis of the 5'-flanking region.";
RL Biochim. Biophys. Acta 1500:323-334(2000).
DR EMBL; AF112242; AAF63858.1; JOINED.
DR EMBL; AF112230; AAF63858.1; JOINED.
DR EMBL; AF112231; AAF63858.1; JOINED.
DR EMBL; AF112232; AAF63858.1; JOINED.
DR EMBL; AF112233; AAF63858.1; JOINED.
DR EMBL; AF112234; AAF63858.1; JOINED.
DR EMBL; AF112235; AAF63858.1; JOINED.
DR EMBL; AF112236; AAF63858.1; JOINED.
DR EMBL; AF112237; AAF63858.1; JOINED.
DR EMBL; AF112238; AAF63858.1; JOINED.
DR EMBL; AF112239; AAF63858.1; JOINED.
DR EMBL; AF112240; AAF63858.1; JOINED.
DR EMBL; AF112241; AAF63858.1; JOINED.
DR EMBL; AF113146; AAF63155.1; JOINED.
DR HSSP; P15848; 1FSU.
DR MGD; MGI:1355303; Galns.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase.1.
DR PROSITE; PS00523; SULFATASE.1; 1.
SQ SEQUENCE 520 AA; 57672 MW; 1F99E31A87A3A365 CRC64;

Query Match 38.2%; Score 47; DB 11; Length 520;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWCKP 17
D 158 GSPNCHFGPYDNKAKP 173

RESULT 14
Q99KJ8 PRELIMINARY; PRT; 520 AA.
ID Q99KJ8
AC Q99KJ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to galactosamine (N-acetyl)-6-sulfate sulfatase.
GN GALNS.
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

Query Match 38.2%; Score 47; DB 5; Length 689;
Best Local Similarity 53.8%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTW 14
D 266 GSSSTRFGPLCWI 278

RESULT 16
Q9FHJ8 PRELIMINARY; PRT; 694 AA.
ID Q9FHJ8
AC Q9FHJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
```


RA Matsui M., Mizuseki K., Nakatani J., Nakanishi S., Sasai Y.;
 RT "Xenopus Kielin: A dorsalizing factor containing multiple chordin-type
 RT repeats secreted from the embryonic midline";
 RL PRC. Natl. Acad. Sci. U.S.A. 97:5291-5296(2000).
 DR EMBL: ASC26192; BAA95483.1; -.
 DR HSSP; P56682; 1CCV.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR002919; TIL_Cysrich.
 DR InterPro: IPR003129; TSPN.
 DR InterPro: IPR001007; VWFC_C.
 DR InterPro: IPR001846; VWFC_D.
 DR Pfam: PF01826; TIL; 1.
 DR Pfam: PF00093; VWC; 22.
 DR Pfam: PF00094; VWD; 1.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC; 27.
 DR SMART; SM00216; VWD; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01208; VWFC; 20.
 SQ SEQUENCE 2327 AA; 255800 MW; 0293109329209993 CRC64;

Query Match 38.2%; Score 47; DB 13; Length 2327;
 Best Local Similarity 57.1%; Pred. No. 2e-02; Mismatches 5; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 5 SCHFGPLTWCKPQ 18
 DB 1823 TCHCKLTWCVHQ 1836

RESULT 20

Q8BVM2 ID Q8BVM2 PRELIMINARY; PRT; 641 AA.
 AC Q8BVM2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created;
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update;
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical proline-rich region/von Willebrand factor type A domain
 DE containing protein.
 DE Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10093;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Testis;
 RX MEDLINE=22354683; PubMed=12466851;
 RA "The FANTCM Consortium.
 RA "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RI Nature 420:563-573(2002).
 DR EMBL; AK077206; BAC36683.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 641 AA; 70415 MW; 199E300730CB85E3 CRC64;

Query Match 37.8%; Score 46.5; DB 11; Length 641;
 Best Local Similarity 61.1%; Pred. No. 66;
 Matches 11; Conservative 0; Mismatches 4; Indels 3; Gaps 2;

QY 5 SCHFGPLTWCKPQ--GGG 20
 DB 487 SCHFMPLVW-CHPKAQQG 503

RESULT 21

Q9FQ67 ID Q9FQ67 PRELIMINARY; PRT; 94 AA.
 AC Q9FQ67;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Resistance protein candidate RGC Ha-1B39 (Fragment).

OS Helianthus annuus (Common sunflower).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 CC Asteridae; Campanulids; Asterales; Asteraceae; Asteroideae;
 CC Heliantheae; Helianthus.
 CX NCBI_TaxID=4232;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21239344; PubMed=11341730;
 RA Gedil M.A., Slabaugh M.B., Berry S., Johnson R., Micheltore R.,
 RA Miller J., Gulya T., Knapp S.J.;
 RT "Candidate disease resistance genes in sunflower cloned using
 RT conserved nucleotide-binding site motifs: genetic mapping and linkage
 RT to the downy mildew resistance gene P11.";
 RL Genome 44:205-212(2001).
 DR EMBL; AF272767; AAG49216.1; -.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00931; NB-ARC; 1.
 FT NON_TER 1 1
 FT NON_TER 94 94
 SQ SEQUENCE 94 AA; 11174 MW; 0C11912DCA83E35D CRC64;

Query Match 37.4%; Score 46; DB 10; Length 94;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 HFGPLTWVC 15
 DB 14 HFEPTWVC 22

RESULT 22

Q08710 ID Q08710 PRELIMINARY; PRT; 240 AA.
 AC Q08710;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Succinate dehydrogenase.
 DE Thermoplasma acidophilum.
 CC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 CC Thermoplasmataceae; Thermoplasma.
 CX NCBI_TaxID=2303;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=122-1B2 AMRC-914;
 RX MEDLINE=93326626; PubMed=8334158;
 RA Bach M., Reilaender H., Gaertner P., Lottspeich F., Michel H.;
 RT "Nucleotide sequence of a putative succinate dehydrogenase operon in
 RT Thermoplasma acidophilum.";
 RL Biochim. Biophys. Acta 1174:103-107(1993).
 DR EMBL; X70908; CAA50262.1; -.
 DR HSSP; P00364; 1KF6.
 DR InterPro; IPR001450; 4Fe4S_ferredoxin.
 DR InterPro; IPR004489; DhsB.
 DR InterPro; IPR001041; Ferredoxin.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00037; fer4; 1.
 DR TIGRFAMs; TIGR00384; dhsB; 1.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; 1.
 KW 4Fe-4S; Iron; Iron-sulfur.
 SQ SEQUENCE 240 AA; 27529 MW; 02164700BA94C55A CRC64;

Query Match 37.4%; Score 46; DB 1; Length 240;
 Best Local Similarity 57.9%; Pred. No. 30;
 Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY 2 GTASCHF-GPLTWCKPQG 19
 DB 198 GTSRCHFACECTVC-PKG 215

RESULT 23

Q9HJG6
 ID Q9HJG6 PRELIMINARY; PRT; 240 AA.
 AC Q9HJG6
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Probable fumarate reductase, subunit B.
 GN TA1002.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 acidophilum.";
 RL Nature 407:508-513 (2000).
 DR EMBL; AL45066; CAC12131.1; -.
 DR HSSP; P00364; 1KF6.
 DR InterPro; IPR001450; 4F84S_ferredoxin.
 DR InterPro; IPR004489; DhsB.
 DR Pfam; PF00111; fer2; 1.
 DR Pfam; PF00037; fer4; 1.
 DR TIGRPFAMS; TIGR00384; dhsB; 1.
 DR PROSITE; PS00198; 4F84S_FERREDOXIN; 1.
 KW Iron-sulfur; Complete D-Totome.
 SQ SEQUENCE 240 AA; 27519 MW; AFC645D16995178B CRC64;

Query Match 37.4%; Score 46; DB 17; Length 240;
 Best Local Similarity 57.9%; Pred. No. 30;
 Matches 11; Conservative 2; Mismatches 4; Indels 2; Gaps 2;

QY 2 GTASCHF-GPLTWCKPQG 19
 ||: ||| | ||: ||
 Db 198 GTSRCHFAGCECTVC-PKG 215

RESULT 24
 G33722
 ID G33722 PRELIMINARY; PRT; 270 AA.
 AC G33722
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Delta-9 desaturase.
 GN DESC.
 OS Spirulina platensis.
 OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
 OX NCBI_TaxID=1156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C1;
 RA Meesapyodsuk D., Deshnum P., Tanticharoen M., Cheevadhanarak S.;
 RT "A genetic study of fatty acid desaturation in cyanobacterium
 RT Spirulina platensis C1: Temperature regulation of desaturase gene
 RT expression.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AJ002065; CAA05166.1; -.
 DR InterPro; IPR001522; Desaturase.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR PRINTS; PR00075; FACDSDATRASE.
 DR ProDom; PD002221; Desaturase; 1.
 SQ SEQUENCE 270 AA; 31406 MW; F4A1DD1576EB6F64 CRC64;

Query Match 37.4%; Score 46; DB 2; Length 270;
 Best Local Similarity 53.8%; Pred. No. 33;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
 ||: ||: ||: ||
 Db 82 GTLACQGGPIQWV 94

RESULT 25
 Q44502
 ID Q44502 PRELIMINARY; PRT; 272 AA.
 AC Q44502
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Delta-9 desaturase (Fatty-acid desaturase).
 GN DESC OR ALL1599.
 OS Anabaena sp. (strain PCC 7120), and
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690, 1172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Anabaena sp. (strain PCC 7120);
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuura A., Muraki A.,
 RA Nakazaki N., Shimpou S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=A. variabilis;
 RX MEDLINE=95014360; PubMed=7929259;
 RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
 RT "Delta 9 Acyl-lipid desaturases of cyanobacteria. Molecular cloning
 RT and substrate specificities in terms of fatty acids, sn-positions, and
 RT polar head groups.";
 RL J. Biol. Chem. 269:25576-25580 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=A. variabilis;
 RX MEDLINE=94207189; PubMed=8155983;
 RA Sakamoto T., Wada H., Nishida I., Ohmori M., Murata N.;
 RT "Identification of conserved domains in the delta 12 desaturases of
 RT cyanobacteria.";
 RL Plant Mol. Biol. 24:643-650 (1994).
 DR EMBL; AP003586; BAB77965.1; -.
 DR EMBL; D14581; BAA03434.1; -.
 DR InterPro; IPR001522; Desaturase.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR PRINTS; PR00075; FACDSDATRASE.
 DR ProDom; PD002221; Desaturase; 1.
 KW Complete proteome.
 SQ SEQUENCE 272 AA; 31418 MW; E2FBD0CB490D0696 CRC64;

Query Match 37.4%; Score 46; DB 16; Length 272;
 Best Local Similarity 53.8%; Pred. No. 33;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
 ||: ||: ||: ||
 Db 82 GTLACQGGPIQWV 94

RESULT 26
 O45177
 ID O45177 PRELIMINARY; PRT; 347 AA.
 AC O45177
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothenical 40.4 kDa protein.
 GN K07H8.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 R: investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX Fulton B., Hawkins J., Gattung S., Wohlmann P., Elliott G.;
 RA "The sequence of C. elegans cosmid K07H8.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047659; AAC04429.1; --
 DR WormPep; K07H8.8; CE18028.
 KW Hypothetical protein.
 SQ SEQUENCE 347 AA; 40403 MW; AB934716F7FA9963 CRC64;

Query Match 37.4%; Score 46; DB 5; Length 347;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ASCHFGPLTWVC 15
 |||||
 DB 24C ADTHFAPQTWVC 251

RESULT 27
 Q8GU51 PRELIMINARY; PRT; 1627 AA.
 AC Q8GU51;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE MRP-like ABC transporter (Fragment).
 GN MRP1.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jasinski M., Ducos E., Martinoia E., Boutry M.;
 RT "The ATP-binding cassette transporters: structure, function and gene
 R: family comparison between rice and Arabidopsis.";
 RL Plant Physiol 0:0-0(0).
 DR EMBL; AJ35215; CAD59448.1; --
 FT NON-TER 1627 1627
 SQ SEQUENCE 1627 AA; 183015 MW; 41635F57BD29AE0E CRC64;

Query Match 37.4%; Score 46; DB 10; Length 1627;
 Best Local Similarity 53.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 FGPLTWCKPQGG 20
 |||||
 DB 3 FQPLEWYQCPVNG 15

RESULT 28
 Q9LT12 PRELIMINARY; PRT; 256 AA.
 AC Q9LT12;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE Gb|AA01580.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsia.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB025633; BAA97250.1; --
 DR SEQUENCE 256 AA; 28518 MW; 613226425F06EBE3 CRC64;

Query Match 37.0%; Score 45.5; DB 10; Length 256;
 Best Local Similarity 47.4%; Pred. No. 38;
 Matches 9; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 GTASCHFGPLTWCKPQGG 20
 |||||
 DB 71 GTTSCNF---EMVCHLEDG 86

RESULT 29
 Q8XZ32 PRELIMINARY; PRT; 289 AA.
 AC Q8XZ32;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE Putative hydrolase protein (EC 3.-.-.-).
 GN RSC1574 OR RS05784.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 CC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 CC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
 RA Sigulier P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissenbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
 RL Nature 415:497-502(2002)
 DR EMBL; AL646065; CA015276.1; --
 DR InterPro; IPR000073; A/B_hydrolase.
 DR InterPro; IPR003089; AB_hydrolase.
 DR InterPro; IPR000379; Ser_estr_site.
 DR Pfam; PF00561; abhydrolase_1.
 DR PRINTS; PR00111; ABHYDROLASE.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 289 AA; 31955 MW; F1A7255A3BA1468A CRC64;

Query Match 37.0%; Score 45.5; DB 16; Length 289;
 Best Local Similarity 44.4%; Pred. No. 42;
 Matches 12; Conservative 1; Mismatches 5; Indels 9; Gaps 2;

QY 3 TASCHFGPLT---W-----VCKPQGG 20
 |||||
 DB 167 TISASFGPHTPEQWRALNTALKPQGG 193
 |||||

RESULT 30

Q8XZ33 Q8XZ33 PRELIMINARY; PRT; 323 AA.
 AC Q8XZ33;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Hypothetical protein R5c1573.
 GN R5c1573 OR R505260.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Ralstoniaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GMT1000;
 RX MEDLINE=21681879; PubMed=118233852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 Chandelier M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,
 Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 Siguiet P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RL Nature 415:497-502(2002).
 DR EMBL; AL646065; CADI5275.1; -;
 DR InterPro; IPR000073; A/b hydrolase.
 DR InterPro; IPR000379; Ser_estrs_site.
 DR Pfam; PF00561; abhydrolase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 323 AA; 35715 MW; C99134AB1216E068 CRC64;

Query Match 37.0%; Score 45.5; DB 16; Length 323;
 Best Local Similarity 44.4%; Pred. No. 47;
 Matches 12; Conservative 1; Mismatches 5; Indels 9; Gaps 2;

QY 3 TASCHFGPLT---W-----VCKPQGG 20
 |||||
 DB 20: TISASFGPHTPEQWRALNTALKPQGG 227
 |||||

RESULT 31

Q9LT13 Q9LT13 PRELIMINARY; PRT; 356 AA.
 AC Q9LT13;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Gb|AA01580.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB025633; BAA97251.1; -;
 SQ SEQUENCE 356 AA; 39393 MW; B4ACB3A0654C7EC0 CRC64;

Query Match 37.0%; Score 45.5; DB 10; Length 356;
 Best Local Similarity 47.4%; Pred. No. 52;
 Matches 9; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 2 GTASCHFGPLTWVCKPQGG 20
 |||||
 DB 107 GTTSCNF---EWVCHLEDG 122
 |||||

RESULT 32

O95965 O95965 PRELIMINARY; PRT; 494 AA.
 AC O95965;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE Ten integrin EGF-like repeat domains protein precursor (ITGBL1).
 GN ITGBL1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung, and Umbilical vein;
 RX MEDLINE=99162403; PubMed=10051402;
 RA Berg R.W., Leung E., Gough S., Morris C., Yao W.P., Wang S.X., Ni J.,
 RA Krissansen G.W.;
 RT "Cloning and characterization of a novel beta integrin-related cDNA
 RT coding for the protein TIED ('ten beta integrin EGF-like repeat
 RT domains') that maps to chromosome band 19q33: A divergent stand-alone
 RT integrin stalk structure.";
 RL Genomics 56:169-178(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22269935; PubMed=12364586;
 RA Chumakov I., Blumenfeld M., Guerassimenco O., Cavarec L., Palicio M.,
 RA Aderrahim H., Bougueleret L., Barry C., Tanaka H., La Rosa P.,
 RA Puech A., Tahri N., Cohen-Akenine A., Delabrosse S., Liessarague S.,
 RA Picard F.-P., Maurice K., Essioux L., Millasseau P., Grel P.,
 RA Debaillet V., Simon A.-M., Caterina D., Dufaire I., Malekzadeh K.,
 RA Belova M., Luan J.-J., Bouillot M., Sambucy J.-L., Prinas G.,
 RA Saumier M., Boubkiri N., Martin-Saumier S., Nasroune M., Feixoto H.,
 RA Delaye A., Pinchot V., Bastucci M., Guillou S., Chevillon M.,
 RA Sainz-Fuertes R., Meguenni S., Aurich-Costa J., Cherif D., Gimalac A.,
 RA Van Duijn C., Gauvreau D., Ouellette G., Fortier I., Realson J.,
 RA Sherbatich T., Riazanskay N., Rogaev E., Raeymaekers P., Aerssens J.,
 RA Konings F., Luyten W., Macchiardi F., Sham P.C., Straub R.E.,
 RA Weinberger D.R., Cohen N., Cohen D.;
 RT "Genetic and physiological data implicating the new human gene G72 and
 RT the gene for D-amino acid oxidase in schizophrenia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13675-13680(2002).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
 CC BONDS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 DR EMBL; AF072752; AAD17666.1; -;
 DR EMBL; AF014302; AAN16024.1; -;
 DR HSP; P05106; IJY2.
 DR InterPro; IPR006209; EGF_like_beta_C.
 DR InterPro; IPR001169; Integrin_beta_C.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR PROSITE; PS00022; EGF_1; 5.
 DR PROSITE; PS01186; EGF_2; 5.
 DR PROSITE; PS00243; INTEGRIN_BETA; 10.
 KW Cell adhesion; Glycoprotein; Integrin; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 494 TEN INTEGRIN EGF-LIKE REPEAT DOMAINS
 FT PROTEIN.
 SQ SEQUENCE 494 AA; 53921 MW; 72E095D0BDAECFF3 CRC64;

Query Match 37.0%; Score 45.5; DB 4; Length 494;

Best Local Similarity 36.7%; Pred. No. 72;
Matches 11; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY 2 GTASCH-----FGPL-----TWVCKPQG 20
DB 72 GVCICHVTEPGMFFGPLCECHEWVCETYDG 101

RESULT 33
Q8VDV0 PRELIMINARY; PRT; 494 AA.

AC Q8VDV0; 494 AA.
DT 01-MAR-2002 (Tremblrel. 20, Created);
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update);
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update);
DE Similar to integrin, beta-like 1 (with EGF-like repeat domains).
CS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RI Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC ! SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC !- PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULFIDE
CC BONDS (BY SIMILARITY).
CC !- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
DR EMBL; BC020152; AAH20152.1; .
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR002049; Laminin_EGF.
DR PRINTS; PR00011; EGFLAMININ.
DR PROSITE; PS00022; EGF 1; 5.
DR PROSITE; PS01186; EGF 2; 5.
DR PROSITE; PS00243; INTEGRIN_BETA; 9.
KW Cell_adhes;cn; Glycoprotein; Integrin; Repeat; Transmembrane.
SQ SEQUENCE 494 AA; 53964 MW; 7F3C53F2EA9949D2 CRC64;

Query Match 37.0%; Score 45.5; DB 11; Length 494;
Best Local Similarity 36.7%; Pred. No. 72;
Matches 11; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY 2 GTASCH-----FGPL-----TWVCKPQG 20
DB 72 GVCICHVTEPGMFFGPLCECHEWVCETYDG 101

RESULT 34
Q8N172 PRELIMINARY; PRT; 546 AA.

AC Q8N172; 546 AA.
DT 01-OCT-2002 (Tremblrel. 22, Created);
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update);
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update);
DE Integrin, beta-like 1 (with EGF-like repeat domains) (Fragment).
CS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strausberg R.;
RI Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036788; AAH36788.1; .
DR Genew; HGNC:6164; ITGBL1.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001169; Integrin_beta_C.
DR PRINTS; PR00011; EGFLAMININ.
DR PROSITE; PS00022; EGF 1; 5.
DR PROSITE; PS01186; EGF 2; 5.

DR PROSITE; PS00243; INTEGRIN_BETA; 10.
FT NON TER 1
SQ SEQUENCE 548 AA; 59518 MW; D407907B2BD4940D CRC64;

Query Match 37.0%; Score 45.5; DB 4; Length 548;
Best Local Similarity 36.7%; Pred. No. 80;
Matches 11; Conservative 1; Mismatches 7; Indels 11; Gaps 2;

QY 2 GTASCH-----FGPL-----TWVCKPQG 20
DB 126 GVCICHVTEPGMFFGPLCECHEWVCETYDG 155

RESULT 35
Q8QUL9 PRELIMINARY; PRT; 79 AA.

AC Q8QUL9; 79 AA.
DT 01-JUN-2002 (Tremblrel. 21, Created);
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update);
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update);
DE ORF090L.
OS Infectious spleen and kidney necrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae;
OX NCBI_TaxID=18017C;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21874810; PubMed=11878892;
RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
RA Chan S.M.;
RT "Complete genome analysis of the mandarin fish infectious spleen and
RT kidney necrosis iridovirus";
RL Virology 29:126-139(2001).
RN [2];
RP SEQUENCE FROM N.A.
RA He J.G., Deng M., Weng S.P., Li Z., Zhou S.Y., Long Q.X., Wang X.Z.,
RA Chan S.M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF371960; AAL98814.1; .
SQ SEQUENCE 79 AA; 9055 MW; F80EC9AC132699B8 CRC64;

Query Match 36.6%; Score 45; DB 12; Length 79;
Best Local Similarity 45.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GGTASCHFGPLTWVCKPQG 20
DB 43 GRQEPCHRGRLMQGAPAGG 62

RESULT 36
Q8YSR8 PRELIMINARY; PRT; 220 AA.

AC Q8YSR8; 220 AA.
DT 01-MAR-2002 (Tremblrel. 20, Created);
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update);
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update);
DE Hypothetical protein A113016.
GN A113016.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120";
RL DNA Res. 8:205-213(2001).

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DR EMBL: AP003591; BAB74715.1; -.
DR InterPro; IPR001601; Methyltransf.
DR Pfam; IPR000051; SAM_bind.
DR InterPro; IPR004033; Ubie/COOS_Metrf.
DR Pfam; PF01209; Ubie_methyltrans; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 220 AA; 24857 MW; 056081B25C43EB90 CRC64;

Query Match 36.6%; Score 45; DB 16; Length 220;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

QY 8 FGPLTWYCKPQGG 20
   : : : : :
Db 131 FAEIKRVCKPQGG 143

RESULT 37
Q8K4K8 PRELIMINARY; PRT; 254 AA.
ID Q8K4K8
AC Q8K4K8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Antioxidant protein.
DE PRDX3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RA Martinez P., Lescuyer P., Rabilloud T., Lunardi J.;
RT "Characterization of the nuclear gene encoding for the mitochondrial
RT antioxidant protein (AOP) from Mus musculus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF333976; AAM74564.1; -.
DR InterPro; IPR000866; AhpC-TSA.
DR Pfam; PF005078; AhpC-TSA; 1.
SQ SEQUENCE 254 AA; 27686 MW; 7CAF1E6592270B99 CRC64;

Query Match 36.6%; Score 45; DB 11; Length 254;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 6; Gaps 0;

QY 7 HFGPLTWYCKPQGG 20
   : : : : :
Db 138 HFSLHAWINTPNGG 151

RESULT 38
Q07873 PRELIMINARY; PRT; 277 AA.
ID Q07873
AC Q07873;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Delta-9 desaturase.
GN DESC.
OS Synchococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97260123; PubMed=9106218;
RA Sakamoto T., Bryant D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
RT acid desaturase genes in the cyanobacterium Synchococcus sp. strain
RT PCC 7002.";
RL Mol. Microbiol. 23:1281-1292(1997).
DR EMBL: U36390; AAB61353.1; -.
DR InterPro; IPR001522; Desaturase.
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DR InterPro; IPR005904; FA_desat_fam.
DR Pfam; PF0487; FA_desaturase; 1.
DR PRINTS; PR00075; FACDSATRASE.
DR ProDom; PD002221; Desaturase; 1.
SQ SEQUENCE 277 AA; 32207 MW; C88FCA8CC1919A48 CRC64;

Query Match 36.6%; Score 45; DB 2; Length 277;
Best Local Similarity 46.2%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWV 14
   : : : : :
Db 82 GTLACQGGPIDWI 94

RESULT 39
Q8LAH5 PRELIMINARY; PRT; 338 AA.
ID Q8LAH5
AC Q8LAH5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Palmitoyl-protein thioesterase-like.
DE Arabidopsis thaliana (Mouse-ear cross).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Haas B.J., Volkovsky N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation.";
RL Genome Biol. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY087806; AAM65342.1; -.
DR InterPro; IPR002472; Palm_thioest.
DR Pfam; PF02089; Palm_thioest; 1.
DR PRINTS; PR00414; PPTHIESTRASE.
SQ SEQUENCE 338 AA; 37136 MW; 10A2369F5AFCCF32 CRC64;

Query Match 36.6%; Score 45; DB 10; Length 338;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTASCHFGPLTWVC 15
   : : : : :
Db 130 GTASIPFRGATWIC 143

RESULT 40
Q9RRJ7 PRELIMINARY; PRT; 370 AA.
ID Q9RRJ7
AC Q9RRJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carboxypeptidase G2.
GN DR2493.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
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RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
RA Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Keschutchan K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioreistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AF002078; AAF12031.1; -.
DR HSSP: P06621; 1CG2.
DR TIGR: DR2493; -.
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam: PF01546; Peptidase_M20; 1.
DR Carboxypeptidase; Complete proteome.
KW Carboxypeptidase; Complete proteome.
SQ SEQUENCE 370 AA; 38831 MW; F45BE553A6694C6D CRC64;

Query Match 36.6%; Score 45; DB 16; Length 370;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTSGHFGP 10
||| |
DB 58 GGTSGHFGP 67

RESULT 41

Q8LJS6 PRELIMINARY; PRT; 373 AA.
AC Q8LJS6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MOC1.
GN MOC1.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN 1;
RP SEQUENCE FROM N.A.
RA Schoenfeld C., Kruse O.;
RT "Identification of a mitf-like protein in Chlamydomonas reinhardtii
RT (MOC1).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF531421; AAM96690.1; -.
DR InterPro: IPR003690; mTERF.
DR Pfam: PF02536; mTERF; 1.
SQ SEQUENCE 373 AA; 40868 MW; FF4654E845E8B479 CRC64;

Query Match 36.6%; Score 45; DB 10; Length 373;
Best Local Similarity 46.7%; Pred. No. 65;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 SCHFGPLTWCKPQG 19

||||| |
DB 358 AAHTGPRRWACEWQG 372

RESULT 42

Q9LGT2 PRELIMINARY; PRT; 534 AA.
AC Q9LGT2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE P0489A01.9 protein.
GN P0489A01.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=4530;
[1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0489A01.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF002484; BAA9518.1; -.
DR Gramene; Q9LGT2; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 1.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS0082; WD_REPEATS_2; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 534 AA; 60503 MW; 44AD91E980DB20BB CRC64;

Query Match 36.6%; Score 45; DB 10; Length 534;
Best Local Similarity 44.4%; Pred. No. 94;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 3 TASCHFGPLTWCKPQG 20
||||| |
DB 276 TMLCHSGPVTAFDRGG 293

RESULT 43

Q9LIEC PRELIMINARY; PRT; 1225 AA.
AC Q9LIEC;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNA-dependent RNA polymerase.
GN POL.
OS Lymantria dispar cypovirus 1.
OC Viruses; dsRNA viruses; Reoviridae; Cypovirus.
OX NCBI_TaxID=165803;
RN 1;
RP SEQUENCE FROM N.A.
RA Rao S., Shapiro M., Lynn D., Hagiwara K., Blackmon B., Fang G.,
RA Carner G.R.;
RT "Identification of dsRNA electrophoretotypes of two cypoviruses from a
RT dual infection in gypsy moth, Lymantria dispar.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF389463; AAK73521.1; -.
DR InterPro: IPR007095; RNA_pol_DS_PS.
DR InterPro: IPR007097; RNA_pol_reo.
DR PROSITE; PS05023; RDRP_REO; 1.
DR PROSITE; PS05021; RDRP_VIRAL; 1.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138845 MW; 614964068B1AB37D CRC64;

Query Match 36.6%; Score 45; DB 12; Length 1225;
Best Local Similarity 63.6%; Pred. No. 21e-02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PLTWCKPQG 20
||||| |
DB 833 PLTWLFPGRGG 843

RESULT 44

Q8B976 PRELIMINARY; PRT; 1225 AA.
ID Q8B976;
AC Q8B976;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNA-dependent RNA polymerase.
OS Dendrolimus punctatus cypovirus 1.

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CC Viruses: dsRNA viruses; Reoviridae; Cypovirus.
CX NCBI_TaxID=208509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao S., Liang C., Hong J., Peng H.;
RT "Dendrolimus punctatus CPV segment 2.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL: AY147187; AAN46860.1; -.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138921 MW; DD480324FCB2A8ED CRC64;

Query Match 36.6%; Score 45; DB 12; Length 1225;
Best Local Similarity 63.6%; Pred. No. 2.le+62;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PLTWCKPQGG 20
DB 833 PLTWLFMPGG 843

RESULT 45
Q8YSJ3 PRELIMINARY; PRT; 1290 AA.
AC Q8YSJ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
DE Two-component hybrid sensor and regulator.
GN AUR3092.
OS Anabaena sp. {strain PCC 7120}.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
CX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Itiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa K., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EXBL: APOC3591; BAB74791.1; -.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_pr_C.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR005467; His_kinase.
DR InterPro: IPR001610; PAC_.
DR InterPro: IPR000700; PAS-assoc_C.
DR InterPro: IPR000014; PAS_domain.
DR InterPro: IPR001789; Response_reg.
DR Pfam: PF02518; HATPase_c; 1.
DR Pfam: PF00512; HiskA; 1.
DR Pfam: PF00785; PAC; 6.
DR Pfam: PF00989; PAC; 5.
DR Pfam: PF00072; response_reg; 1.
DR PRINTS: PR00344; BCTRLSENSOR.
DR ProDom: PD000039; Response_reg; 1.
DR SMART: SM00387; HATPase_c; 1.
DR SMART: SM00388; HiskA; 1.
DR SMART: SM00086; PAC; 6.
DR SMART: SM00091; PAS; 5.
DR SMART: SM00448; REC; 1.
DR TIGRFS: TIGR00229; sensory_box; 6.
DR PROSITE: PS50109; HIS_KIN; 1.
DR PROSITE: PS0113; PAC; 6.
DR PROSITE: PS0112; PAS; 5.
DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
KW Complete proteome.
SQ SEQUENCE 1290 AA; 144892 MW; FC0BDC7CBDE8E2B2 CRC64;

Query Match 36.6%; Score 45; DB 16; Length 1290;
Best Local Similarity 63.6%; Pred. No. 2.le+62;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

CC Viruses: dsRNA viruses; Reoviridae; Cypovirus.
CX NCBI_TaxID=208509;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhao S., Liang C., Hong J., Peng H.;
RT "Dendrolimus punctatus CPV segment 2.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RW EMBL: AY147187; AAN46860.1; -.
KW RNA-directed RNA polymerase.
SQ SEQUENCE 1225 AA; 138921 MW; DD480324FCB2A8ED CRC64;

Query Match 36.6%; Score 45; DB 10; Length 1494;
Best Local Similarity 37.5%; Pred. No. 2.6e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 GOTASCHFGPLTWCK 16
DB 290 GGGGCGYRAVSWLCK 305

RESULT 47
Q9C8G9 PRELIMINARY; PRT; 1622 AA.
AC Q9C8G9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Glutathione S-conjugate transporting ATPase (AtMRP1).
GN T4K22.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucoide II; Brassicales; Brassicaceae; Arabidopsids.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

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RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 438:816-920(2000).
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AC025295; AAGS1096.1; .
 DR InterPro; IPR003593; AAA_Atpase.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1622 AA; 181925 MW; B71E085798F1B506 CRC64;

Query Match 36.6%; Score 45; DB 10; Length 1622;
 Best Local Similarity 70.0%; Pred. No. 2.8e-02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 8 FGPLTWVCKP 17
 Db 3 FEPLDWYCKP 12

RESULT 48
 Q24635 PRELIMINARY; PRT; 1622 AA.
 AC Q24635;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created);
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE Multidrug resistance-associated protein homolog.
 GN MRPI.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97368351; PubMed=9223346;
 RA Lu Y.-P., Li Z.-S., Rea P.A.;
 RT "AtMRPI Gene of Arabidopsis encodes a putative ABC-transporter pump;
 RT isolation and functional definition of a putative ATP-binding cassette
 transporter gene";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:824-828(1997).
 RN [2]

Query Match 36.6%; Score 45; DB 10; Length 1622;
 Best Local Similarity 70.0%; Pred. No. 2.8e-02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 8 FGPLTWVCKP 17
 Db 3 FEPLDWYCKP 12

RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana";
 RL Nature 438:816-920(2000).
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AC025295; AAGS1096.1; .
 DR InterPro; IPR003593; AAA_Atpase.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1622 AA; 181925 MW; B71E085798F1B506 CRC64;

Query Match 36.6%; Score 45; DB 5; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 5e-02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 8 FGPLTWVCKP 17
 Db 3 FEPLDWYCKP 12

RESULT 49
 Q26008 PRELIMINARY; PRT; 2910 AA.
 AC Q26008;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created);
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE RNA polymerase I.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Honduras I;
 RX MEDLINE=94081864; PubMed=8259131;
 RA Fox B.A., Li W.B., Tanaka M., Inselburg J., Bzik D.J.;
 RT "Molecular characterization of the largest subunit of plasmodium
 falciparum RNA polymerase I";
 RL Mol. Biochem. Parasitol. 61:37-48(1993).
 DR EMBL; L11172; AAA72349.1; .
 DR InterPro; IPR006592; RNA_polA_N.
 DR InterPro; IPR000722; RNA_pol_A.
 DR InterPro; IPR007080; RNA_pol_Rpb1_1.
 DR InterPro; IPR007066; RNA_pol_Rpb1_3.
 DR InterPro; IPR007083; RNA_pol_Rpb1_4.
 DR InterPro; IPR007081; RNA_pol_Rpb1_5.
 DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.
 DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.
 DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.
 DR SMART; SM00663; RPOA_N; 1.
 SQ SEQUENCE 2910 AA; 34070 MW; AF838248497DAB22 CRC64;

Query Match 36.6%; Score 45; DB 5; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 5e-02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 7 HFGPLTWVCK 16
 Db 2702 HFSPVTWIK 2711

RESULT 50
 Q81410 PRELIMINARY; PRT; 2914 AA.
 AC Q81410;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update);
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update);
 DE RNA polymerase I.
 GN PFE0465C
 OS Plasmodium falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
 RA Hall N., Bowman S., Churcher C., Quail M., Barrell B.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]

Query Match 36.6%; Score 45; DB 5; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 5e-02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 7 HFGPLTWVCK 16
 Db 2702 HFSPVTWIK 2711

RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Suiston J.E., Craig A., Newbold C., Barrell B.G.;
RI "Sequence of Plasmidium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL; AL929352; CAD51459.1; -.
SQ SEQUENCE 2914 AA; 340672 MW; 7ED0547CCBF376EE CRC64;

Query Match 36.6%; Score 45; DB 5; Length 2914;
Best Local Similarity 60.0%; Pred. No. 5.1e-02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 HFGPLTWCK 16
|||.|.|.|.
Db 2703 HFSPVTWIK 2712

Search completed: November 5, 2003, 19:06:45
Job time : 38 secs